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(54) Title: MAMMALIAN MIXED LYMPHOCYTE RECEPTORS, CHEMOKINE RECEPTORS [MMLR-CCR]			
(57) Abstract The present invention provides polynucleotides (mmlr-ccr or mpbg-ccr) which encode novel chemokine receptors (MMLR-CCR or MPBG-CCR). The present invention provides for screening methods for the detection of molecules that modulate receptor activity. The present invention also provides for antisense molecules, diagnostic molecules, genetically engineered expression vectors and host cells for the production of purified MMLR-CCR or MPBG-CCR; antibodies, agonists, antagonists and inhibitors of MMLR-CCR or MPBG-CCR; and pharmaceutical compositions and methods of treatment based on the polypeptide, its antibodies, antagonists and inhibitors. The invention further provides diagnostic and therapeutic compositions for the detection and treatment of infection, inflammation, proliferative disease, solid tumors and cardiovascular disease.			

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MAMMALIAN MIXED LYMPHOCYTE RECEPTORS. CHEMOKINE RECEPTORS [MMLR-CCR]

TECHNICAL FIELD

5 The present invention relates generally to the field of molecular biology and specifically to novel nucleotide and amino acid sequences of two chemokine receptors. The present invention further relates to the use of the novel nucleotide and amino acid sequences disclosed herein in the diagnosis and treatment of disease.

BACKGROUND ART

10 The chemokines are small, chemotactic polypeptides, generally about 70-100 amino acids in length, 8-11 kD in molecular weight and active over a 1-100 ng/ml concentration range, that mediate the migration of leukocytes toward sites of infection. Initially, they were isolated and purified from inflamed tissues and characterized relative to their bioactivity. More recently, chemokines have been discovered through molecular cloning techniques and characterized by
15 structural as well as functional analysis.

The chemokines are related through both primary structure and the presence of a cysteine motif which is based primarily on the spacing of the first two cysteine residues in the mature molecule. Currently the chemokines are assigned to one of two families, the C-X-C chemokines (α) and the C-C chemokines (β). Although exceptions exist, the C-X-C chemokines generally
20 activate neutrophils and fibroblasts while the C-C chemokines act on a more diverse group of target cells which include monocytes/macrophages, basophils, eosinophils, T lymphocytes and others. The C-X-C class includes melanoma growth-stimulating activity (MGSA), interleukin-8 (IL-8) and neutrophil-activating peptide 2 (NAP-2). The C-C class includes RANTES (Regulated on Activation, Normal T Expressed and Secreted), macrophage inflammatory protein-
25 1α and 1β (MIP- 1α and 1β) and monocyte chemoattractant protein-1 (MCP-1).

MCP-1 is a potent and specific monocyte agonist and chemoattractant that is produced by endothelial cells, smooth muscle cells, and macrophages in response to mediators including platelet-derived growth factor, tumor necrosis factor α , lipopolysaccharide and oxidized low density lipoproteins. MCP-1 has been implicated in mediating monocyte infiltration of tissues in
30 inflammatory diseases, such as rheumatoid arthritis, alveolitis, atherosclerosis, and macrophage infiltration of tumors where it may be involved in the suppression of tumor growth in animal models (Charo (1994) Proc Natl Acad Sci 91:2752-2756). Charo (supra) reports that monocyte invasion in the artery wall is a critical event in the initiation of atherosclerosis and that MCP-1 is

other related proteins (MCP-2 and MCP-3) were purified from a human osteosarcoma cell line and have 62% and 73% amino acid identity, respectively, with MCP-1 and share its chemoattractant specificity for monocytes.

In addition to leukocyte trafficking, both C-C and C-X-C chemokines are implicated as major participants in acute as well as chronic inflammatory conditions. inhibition of hematopoiesis, modulation of angiogenesis and fibroplasia (Taub et al (1994) *Ther Immunol* 1:229-246). Macrophage inflammatory protein 1 alpha (MIP-1 α) has been reported to inhibit proliferation of hematopoietic stem cells *in vitro* and *in vivo* (Cook J 1996 *Leukoc Biol* 59:61-66), and Gewirtz et al (1995; *Blood* 86:2559-2567) report that three C-C chemokines, MIP-1 α and MIP-1 β and c10, specifically inhibited megakaryocyte colony formation at neutrophil activating peptide-2 (NAP-2) equivalent doses. Eaves et al (1993 *Proc Natl Acad Sci USA* 90:12015-12019) suggest the administration of MIP-1 α to patients with chronic myeloid leukemia (CML) for the protection of primitive normal myeloid cells.

Chemokines produce their biological effects by interacting with specific receptors on the cell surface of their target cells, i.e., immune cells. The known chemokine receptors are basic proteins that internalize after binding and are coupled to G-proteins. Additionally, they display amino acid sequences which are predicted to conform to an architecture containing seven-transmembrane spanning segments connected by a series of intra- and extracellular loops. C-X-C and CC chemokine receptors are highly specific and there is no cross-competition for binding between the two different classes of chemokines. The exception to the rule is the erythrocyte chemokine receptor that binds both C-C and C-X-C chemokines with high affinity and has been shown to be a receptor for the malarial parasite, *Plasmodium vivax*. There are features of the erythrocyte chemokine receptor that distinguish it from the previously characterized receptors, however. The erythrocyte chemokine receptor is an acidic protein that does not internalize after binding and is not regulated by G proteins (Horuk (1994) *Trends Pharmacol Sci* 15:159-165).

At least two C-X-C chemokine receptors, IL8 α and IL8 β , have been reported by Holmes et al (1991 *Science* 253:1278-1280) and Murphy et al (1991; *Science* 253:1280-1283), respectively. Three C-C receptor types, the MIP-1 α /RANTES type (CCR-1), the MCP-1 type (CCR-2) and CCR-3 (initially derived from murine eosinophils) have been reported (Post et al (1995) *J Immunol* 155:5299-305). Charo (supra) reports on the cloning of two MCP-1 receptor isoforms that are most closely related to the MIP-1 α receptor. He also reports on the presence of the amino acid sequence, IFFIILLTIDRYLAIVHAVFAL(K/R)ARTVFGV, in the MCP-1 receptors. The sequence occurs in the third transmembrane domain and second intracellular loop and is

known to interact with G-binding proteins in rhodopsin. Charo (supra) suggests that this domain may mediate aspects of G-protein activation common to receptors for C-C chemokines.

The discovery of new chemokine receptors associated with monocyte/macrophage chemotaxis will provide the basis for the development of new methods for screening for modulators of receptor activity and will aid in the development of diagnostic and therapeutic agents for inflammation, infection and conditions associated with abnormal proliferation of cells.

DISCLOSURE OF THE INVENTION

The present invention relates to a novel chemokine receptor, designated herein as MMLR-CCR. The nucleotide sequence encoding MMLR-CCR was found among the sequences of a cDNA library made from plastic adherent mononuclear cells collected on day two of a two-way mixed lymphocyte (MLR) culture. The present invention also relates to a novel chemokine receptor, designated herein as MPHG-CCR. The nucleotide sequence encoding MPHG-CCR was found among the sequences of a cDNA library made from plastic adherent (two hour culture) mononuclear cells. The present invention relates to the use of the nucleotide and amino acid sequences for the two chemokine receptors disclosed herein in the study, diagnosis and treatment of disease states in which normal leukocyte functioning is perturbed by either normal leukopoiesis or by inappropriate activation via chemokine agonists or antagonists, such as in infection, inflammation, proliferative diseases, tumorigenesis, and cardiovascular disease.

The present invention also relates to the use of mmlr-ccr and mphg-ccr and genetically engineered host cells that express MMLR-CCR and MPHG-CCR to evaluate, screen and identify 1) the naturally occurring, biological ligands, i.e. chemokines, in appropriate cellular supernatants and 2) substances, compounds or synthetic drugs that modulate receptor activation, by modulating receptor/ligand binding, thereby modulating signal transduction events. Such genetically engineered host cells could be used, for example, to screen peptide libraries or organic molecules capable of modulating receptor/ligand binding.

The present invention is based in part on the amino acid homology that MMLR-CCR shares with the MCP-1 CCR-2 chemokine receptor, MCP-1RB, disclosed in GenBank, NCBI gi: 472558 (Charo, supra) and the amino acid homology that MPHG-CCR shares with C-C chemokine receptor 3 (g881570) and MCP-1RA receptor (g472556) disclosed in Charo (supra). In particular, MMLR-CCR contains the conserved amino acid sequence IFFIILLTIDRYLAV VHAVFAL(K/R)ARTVFGV found in the third transmembrane domain and second intracellular loop of chemokine receptors which in the corresponding region of rhodopsin is known to participate in G-protein binding, suggesting that this domain may mediate aspects of G-protein

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activation common to receptors for C-C chemokines. There is one conserved amino acid substitution in the G-protein binding domain at position 121 in MMLR-CCR which is valine instead of isoleucine as is reported by Charo (supra).

The present invention is therefore based on the discovery of two novel C-C chemokine
 5 receptors, MMLR-CCR and MPH-CCR, that may be associated with monocyte/macrophage
 infiltration and chemotaxis and hematopoiesis. MMLR-CCR and MPH-CCR and nucleotide
 sequences that encode them and oligonucleotides, peptide nucleic acid (PNA), fragments,
 portions or antisense molecules thereof, provide the basis for diagnostic methods for the detection
 and/or quantitation of a MMLR-CCR associated with infection, inflammation, proliferative
 10 diseases, tumorigenesis, and cardiovascular disease, including such diseases as rheumatoid
 arthritis; alveolitis; atherosclerosis; chronic granulomatous disease (characterized by an extensive
 inflammatory reaction); asthma; autoimmune diseases, such as myasthenia gravis, diabetes and
 inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome
 (characterized by decreased microbicidal killing); conditions associated with abnormal
 15 proliferation of cells; and solid tumors. For example, the mmlr-ccr nucleotide sequence disclosed
 herein, which encodes MMLR-CCR, or fragments thereof, may be used in hybridization assays
 of biopsied cells or tissues or bodily fluids to detect mmlr-ccr nucleic acid which may be
 associated with such disease states.

An abnormal level of mmlr-ccr or mphg-ccr nucleotide sequences or an abnormal
 20 transcript size in a biological sample may be characteristic of a regulatory state in which the
 receptors are over-expressed or under-expressed. Nucleotide sequences encoding MMLR-CCR
 or MPH-CCR provide the basis for probes which can be used diagnostically to detect
 chromosomal aberrations such as deletions, mutations or chromosomal translocations in the gene
 encoding the chemokine receptors. Gene expression may be altered in such disease states or
 25 there may be a chromosomal aberration present in the region of the gene encoding the receptor.

The present invention also relates, in part, to expression vectors and genetically
 engineered host cells comprising nucleotide sequences encoding MMLR-CCR or MPH-CCR
 for in vitro or in vivo production of the nucleotide sequences.

Additionally, the present invention relates to the use of a MMLR-CCR or MPH-CCR
 30 polypeptide, or fragment or variant thereof, to produce antibodies and to screen for antagonists or
 inhibitors of the chemokine receptors which can be used diagnostically to detect and quantitate
 protein levels in disease states.

Peptides or small molecules capable of modulating receptor levels or activity will provide

the basis for pharmaceutical compositions for the treatment of disease states associated with receptor activation, such as inflammation. Chemokine receptor antisense molecules may be used to down-regulate the presence of the receptor on the cell surface in conditions where it is preferable to decrease receptor signaling. Alternatively, antagonists of the chemokine receptor/ligand interaction may be used to block receptor/ligand binding in diseases or conditions where it is preferable to block or reduce receptor activation. i.e., signal transduction events which lead to infiltration/chemotaxis, and a variety of other second messenger mediated cellular events. Alternatively, mmlr-ccr or mphg-ccr sense molecules may be used to up-regulate the presence of the receptor and MMLR-CCR or MPHG-CCR agonists may be used to enhance receptor activation thereby enhancing signal transduction events in conditions where it is desirable to increase chemotaxis and other second messenger mediated cellular events. Such molecules capable of modulating receptor activity can be administered alone or in combination with other therapeutics for the treatment of diseases.

The invention further provides diagnostic assays and kits for the detection of MMLR-CCR or MPHG-CCR in cells and tissues comprising one of the purified receptors which may be used as a positive control, and anti-receptor antibodies. Such antibodies may be used in solution-based, membrane-based, or tissue-based technologies to detect any disease state or condition related to the expression of protein or expression of deletions or variants thereof.

BRIEF DESCRIPTION OF DRAWINGS

Figures 1A-D display the polynucleotide (SEQ ID NO:1) and deduced amino acid (SEQ ID NO:2) sequence for MMLR-CCR. The conserved sequence IFFILLTIDRYLAV VHAVFAL(K/R)ARTVFGV begins at amino acid residue 107.

Figures 2A-B display the amino acid alignment of MMLR-CCR and the MCP-1 receptor (Charo, supra). Sequences shown in this Figure and Figure 7 were produced using the multisequence alignment program of DNASTAR software (DNASTAR Inc, Madison WI).

Figure 3 displays an analysis of the hydrophobicity characteristics of MMLR-CCR based on the predicted amino acid sequence.

Figure 4 displays the isoelectric point for MMLR-CCR [pI=9.69] as determined by MacDNAsis.

Figure 5 displays the results of northern blot analysis using Incyte Clone 478861 which encodes MMLR-CCR, as a probe.

Figures 6A-C display the polynucleotide (SEQ ID NO:3) and deduced amino acid (SEQ ID NO:4) sequence for MPHG-CCR.

Figures 7A-B display the amino acid alignments of MPHG-CCR with the C-C chemokine receptor (GI 881570).

Figure 8 displays an analysis of the hydrophobicity characteristics of MPHG-CCR based on the predicted amino acid sequence.

Figure 9 displays the isoelectric point for MPHG-CCR as determined by MacDNAsis. The results indicate that the isoelectric point [pI] for MPHG-CCR is 7.63.

MODES FOR CARRYING OUT THE INVENTION

The present invention relates to a novel chemokine receptor, designated herein as MMLR-CCR, the nucleotide sequence of which was initially found among the sequences of a cDNA library made from mononuclear cells collected on day two of a mixed lymphocyte (MLR) culture. The present invention also relates to a novel chemokine receptor, designated herein as MPHG-CCR, the nucleotide sequence of which was initially found among the sequences of a cDNA library made from mononuclear cells. The present invention relates to the use of the nucleotide and amino acid sequences disclosed herein in the study, diagnosis and treatment of disease states in which normal leukocyte functioning is perturbed by either by normal leukopoiesis or by inappropriate activation via chemokine agonists or antagonists, such as in infection, inflammation, proliferative diseases, tumorigenesis, and cardiovascular disease.

The present invention also relates to the use of MMLR-CCR and MPHG-CCR and genetically engineered host cells that express MMLR-CCR and MPHG-CCR to evaluate, screen and identify 1) the naturally occurring, biological ligands, i.e. chemokines, in appropriate cellular supernatants and 2) substances, compounds or synthetic drugs that modulate receptor activation, by modulating receptor/ligand binding, thereby modulating signal transduction events.

The present invention is based in part on the presence of nucleotide sequences encoding MMLR-CCR in random samples of 5654 usable sequences in a cDNA library made from monocytes of a 48 hour treated mixed lymphocyte culture, i.e. cells associated with inflammation and immunomodulation. Nucleotide sequences for MMLR-CCR are absent in a random sample of 7749 usable sequences in a cDNA library made from monocytes not subjected to a mixed lymphocyte reaction. The present invention is also based in part on the presence of nucleotide sequences encoding MPHG-CCR in random samples of 7749 usable sequences in a cDNA library made from monocytes not subjected to a mixed lymphocyte reaction. As used herein the term "usable sequences" refers to the total number of clones in a library after the removal of vector, nucleotide repeats, contamination, and mitochondrial DNA. The present invention is further based in part on the amino acid homology that MMLR-CCR shares with the known MCP-

1 chemokine receptor, MCP-IRB (GenBank accession number gi: 472558), and the presence of the conserved amino acid motif associated with G protein binding and the amino acid homology that MPHG-CCR shares with C-C chemokine receptor 3 and MCP-IRA.

The present invention therefore is based upon the identification of novel chemokine
5 receptors, MMLR-CCR and MPHG-CCR, that are associated with disease states in which normal leukocyte functioning is perturbed by either normal leukopoiesis or by inappropriate activation by chemokine agonists or antagonists, such as in infection, inflammation, proliferative diseases, tumorigenesis and cardiovascular disease, including rheumatoid arthritis; alveolitis;
atherosclerosis; chronic granulomatous disease (characterized by an extensive inflammatory
10 reaction); asthma; autoimmune diseases, such as, myasthenia gravis, diabetes and inflammatory bowel disease; toxic shock syndrome; septic shock; Chediak-Higashi syndrome (characterized by decreased microbicidal killing); and conditions associated with abnormal proliferation of cells, such as tumorigenesis.

"Nucleic acid sequence" as used herein refers to an oligonucleotide, nucleotide or
15 polynucleotide sequence, and fragments or portions thereof, and to DNA or RNA of genomic or synthetic origin which may be double-stranded or single-stranded, whether representing the sense or antisense strand. As used herein "amino acid sequence" refers to peptide or protein sequences or portions thereof. As used herein, lower case "mmlr-ccr" or "mphg-ccr" refers to a nucleic acid sequence whereas upper case "MMLR-CCR" and "MPHG-CCR" refers to a protein sequence.
20 As used herein, peptide nucleic acid (PNA) refers to a class of informational molecules that have a neutral "peptide like" backbone with nucleobases that allow molecules to hybridize to complementary DNA or RNA with higher affinity and specificity than corresponding oligonucleotides (PerSeptive Biosystems 1-800-899-5858).

As used herein, MMLR-CCR and MPHG-CCR encompasses MMLR-CCR and MPHG-
25 CCR, respectively, from any mammalian species, including bovine, ovine, murine, porcine, equine and preferably human sources, in naturally occurring or in variant form, or from any source, whether natural, synthetic, semi-synthetic or recombinant.

As used herein, "naturally occurring" refers to a MMLR-CCR or MPHG-CCR with an amino acid sequence found in nature, and "biologically active" refers to MMLR-CCR or MPHG-
30 CCR having structural, regulatory or biochemical functions of the naturally occurring receptors. As used herein, "immunological activity" is defined as the capability of the natural, recombinant or synthetic MMLR-CCR or MPHG-CCR or any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The term "derivative" as used herein refers to the chemical modification of MMLR-CCR or MPH-CCR. Illustrative of such modifications is replacement of hydrogen by an alkyl, acyl, or amino group. A chemokine receptor derivative retains essential biological characteristics of the naturally occurring chemokine receptor.

- 5 As used herein, the term "purified" refers to molecules, either nucleic or amino acid sequences, that are removed from their natural environment and isolated or separated from at least one other component with which they are naturally associated.

The Coding Sequences

- The nucleotide sequences of human mmlr-ccr (SEQ ID NO:1) and human mphg-ccr are shown in Figures 1A-D and 6A-C, respectively. A partial coding region for mmlr-ccr was identified within a cDNA library made from MMLR cells where it was found one time in 5654 usable sequences. A partial coding region for mphg-ccr was identified within a cDNA library made from macrophages where it was found one time in 7749 usable sequences. A BLAST search (Basic Local Alignment Search Tool; Altschul SF (1993) J Mol Evol 36: 290-300; Altschul SF et al (1990) J Mol Biol 215:403-410) comparing the human MCP-1 receptor (NCBI GI 472558) against the cDNAs of the MMLR library (Incyte library MMLR2DT01) identified Incyte Clone 478861 (mmlr-ccr) and 442279 (mphg-ccr). The 5' nucleotide region of mmlr-ccr and mphg-ccr was obtained through PCR extension and sequenced.

- The nucleotide sequence of SEQ ID NO:1 encodes a MMLR-CCR amino acid sequence (SEQ ID NO:2) having 332 amino acid residues with the domain, IFFIILLTIDRYLAV VHAFAL(K/R)ARTVFGV occurring at residue positions 107-128, inclusive, of SEQ ID NO:2. As illustrated in Figure 3, MMLR-CCR contains seven-transmembrane spanning segments connected by a series of intracellular and extracellular loops. The nucleotide sequence of SEQ ID NO:3 encodes a MPH-CCR amino acid sequence (SEQ ID NO: 4) having 344 amino acid residues.

- Methods for DNA sequencing are well known in the art and employ such enzymes as the Klenow fragment of DNA polymerase I, Sequenase® (US Biochemical Corp, Cleveland OH)), Taq polymerase (Perkin Elmer, Norwalk CN), thermostable T7 polymerase (Amersham, Chicago IL), or combinations of recombinant polymerases and proofreading exonucleases such as the ELONGASE Amplification System marketed by Gibco/BRL (Gaithersburg MD). Methods to extend the DNA from an oligonucleotide primer annealed to the DNA template of interest have been developed for both single-stranded and double-stranded templates. Chain termination reaction products were separated using electrophoresis and detected via their incorporated,

labeled precursors. Recent improvements in mechanized reaction preparation, sequencing and analysis have permitted expansion in the number of sequences that can be determined per day. Preferably, the process is automated with machines such as the Hamilton Micro Lab 2200 (Hamilton, Reno NV), Peltier Thermal Cycler (PTC200; MJ Research, Watertown MA) and the ABI Catalyst 800 and 377 and 373 DNA sequencers (Perkin Elmer, Norwalk CN).

The quality of any particular cDNA library in which polynucleotides encoding the chemokine receptors are found may be determined by performing a pilot scale analysis of the cDNAs and checking for percentages of clones containing vector, lambda or *E. coli* DNA, mitochondrial or repetitive DNA, and clones with exact or homologous matches to public databases.

Extending Receptor Polynucleotide Sequences

The polynucleotide sequence encoding MMLR-CCR or MPHG-CCR may be extended utilizing the nucleotide sequences from SEQ ID NO:1 or SEQ ID NO:3, respectively, in various methods known in the art to detect upstream sequences such as promoters and regulatory elements. Sarkar G et al (1993; PCR Methods Applic 2:318-22) disclose "restriction-site polymerase chain reaction (PCR)" as a direct method which uses universal primers to retrieve unknown sequence adjacent to a known locus. First, genomic DNA is amplified in the presence of primer to a linker sequence and a primer specific to the known region. The amplified sequences are subjected to a second round of PCR with the same linker primer and another specific primer internal to the first one. Products of each round of PCR are transcribed with an appropriate RNA polymerase and sequenced using reverse transcriptase.

Inverse PCR can be used to amplify or extend sequences using divergent primers based on a known region (Triglia T et al (1988) Nucleic Acids Res 16:8186). The primers may be designed using Oligo 4.0 (National Biosciences Inc, Plymouth MN), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. The method uses several restriction enzymes to generate a suitable fragment in the known region of a gene. The fragment is then circularized by intramolecular ligation and used as a PCR template.

Capture PCR (Lagerstrom M et al (1991) PCR Methods Applic 1:111-19) is a method for PCR amplification of DNA fragments adjacent to a known sequence in human and yeast artificial chromosome (YAC) DNA. Capture PCR also requires multiple restriction enzyme digestions and ligations to place an engineered double-stranded sequence into an unknown portion of the DNA molecule before PCR.

Parker JD et al (1991; Nucleic Acids Res 19:3055-60), teach walking PCR, a method which permits retrieval of unknown sequence. PromoterFinder™ is a new kit available from Clontech (Palo Alto CA) which uses PCR, nested primers and special libraries to "walk in" genomic DNA. This process avoids the need to screen libraries and is useful in finding
5 intron/exon junctions.

Another PCR method, "Improved Method for Obtaining Full Length cDNA Sequences" by Guegler et al, Patent Application Serial No 08/487,112, filed June 7, 1995 and hereby incorporated by reference, employs XL-PCR™ enzymes (Perkin-Elmer, Foster City CA) to amplify and/or extend nucleotide sequences.

10 Preferred libraries for screening for full length cDNAs are ones that have been size-selected to include larger cDNAs. Also, random primed libraries are preferred in that they will contain more sequences which contain the 5' and upstream regions of genes. A randomly primed library may be particularly useful if an oligo d(T) library does not yield a full-length cDNA. Genomic libraries are useful for obtaining introns and extending 5' sequence.

15 A new method for analyzing either the size or confirming the nucleotide sequence of sequencing or PCR products is capillary electrophoresis. Systems for rapid sequencing are available from Perkin Elmer, Beckman Instruments (Fullerton CA), and other companies. Capillary sequencing employs flowable polymers for electrophoretic separation, four different fluorescent dyes (one for each nucleotide) which are laser activated, and detection of the emitted
20 wavelengths by a charge coupled device camera. Output/light intensity is converted to electrical signal using appropriate software (eg. Genotyper™ and Sequence Navigator™ programs from Perkin Elmer) and the entire process from loading of samples to computer analysis and electronic data display is computer controlled. Capillary electrophoresis is particularly suited to the sequencing of small pieces of DNA which might be present in limited amounts in a particular
25 sample. The reproducible sequencing of up to 350 bp of M13 phage DNA in 30 min has been reported (Ruiz-Martinez MC et al (1993) Anal Chem 65:2851-8).

Expression Systems

In accordance with the present invention, mmlr-ccr or mphp-ccr polynucleotide sequences which encode MMLR-CCR or MPHP-CCR, fragments of the polypeptide, fusion proteins or
30 functional equivalents thereof, may be used to generate recombinant DNA molecules that direct the expression of MMLR-CCR or MPHP-CCR in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence, may be used to clone and express MMLR-CCR or

MPHG-CCR. As will be understood by those of skill in the art, it may be advantageous to produce chemokine receptor-encoding nucleotide sequences possessing non-naturally occurring codons. Codons preferred by a particular prokaryotic or eukaryotic host (Murray E et al (1989) Nuc Acids Res 17:477-508) can be selected, for example, to increase the rate of expression or to produce recombinant RNA transcripts having desirable properties, such as a longer half-life, than transcripts produced from naturally occurring sequence.

Also included within the scope of the present invention are polynucleotide sequences that are capable of hybridizing to the nucleotide sequence of Figure 1A-D or Figure 6A-C under conditions of intermediate to maximal stringency. Hybridization conditions are based on the melting temperature (T_m) of the nucleic acid binding complex, as taught in Berger and Kimmel (1987, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol 152, Academic Press, San Diego CA) incorporated herein by reference, and confer a defined "stringency" as explained below.

"Maximum stringency" typically occurs at about $T_m - 5^\circ\text{C}$ (5°C below the T_m of the probe); "high stringency" at about 5°C to 10°C below T_m ; "intermediate stringency" at about 10°C to 20°C below T_m ; and "low stringency" at about 20°C to 25°C below T_m . As will be understood by those of skill in the art, a maximum stringency hybridization can be used to identify or detect identical polynucleotide sequences while an intermediate (or low) stringency hybridization can be used to identify or detect similar or related polynucleotide sequences. The term "hybridization" as used herein shall include "the process by which a strand of nucleic acid joins with a complementary strand through base pairing" (Coombs J (1994) Dictionary of Biotechnology, Stockton Press, New York NY) as well as the process of amplification has carried out in polymerase chain reaction technologies as described in Dieffenbach CW and GS Dveksler (1995, PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview NY) and incorporated herein by reference.

As used herein a "deletion" is defined as a change in either nucleotide or amino acid sequence in which one or more nucleotides or amino acid residues, respectively, are absent.

As used herein an "insertion" or "addition" is that change in a nucleotide or amino acid sequence which has resulted in the addition of one or more nucleotides or amino acid residues, respectively, as compared to the naturally occurring MMLR-CCR or MPHG-CCR.

As used herein "substitution" results from the replacement of one or more nucleotides or amino acids by different nucleotides or amino acids, respectively.

Altered MMLR-CCR or MPHG-CCR polynucleotide sequences which may be used in

accordance with the invention include deletions, insertions or substitutions of different nucleotide residues resulting in a polynucleotide that encodes the same or a functionally equivalent MMLR-CCR or MPH-G-CCR. The protein may also show deletions, insertions or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent receptors.

- 5 Deliberate amino acid substitutions may be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues as long as the biological activity of the receptor is retained. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values
- 10 include leucine, isoleucine, valine; glycine, alanine; asparagine, glutamine; serine, threonine, phenylalanine, and tyrosine.

- Included within the scope of the present invention are alleles of MMLR-CCR or MPH-G-CCR. As used herein, an "allele" or "allelic sequence" is an alternative form of MMLR-CCR or MPH-G-CCR. Alleles result from a mutation, i.e., a change in the nucleic acid sequence, and
- 15 generally produce altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to deletions, additions or substitutions of amino acids. Each of these types of changes may occur alone, or in combination with the others, one or more times in a given sequence.

- 20 The nucleotide sequences of the present invention may be engineered in order to alter a MMLR-CCR or MPH-G-CCR coding sequence for a variety of reasons, including but not limited to, alterations which modify the cloning, processing and/or expression of the gene product. For example, mutations may be introduced using techniques which are well known in the art, e.g., site-directed mutagenesis to insert new restriction sites, to alter glycosylation patterns, to change
- 25 codon preference, etc.

- In another embodiment of the invention, a MMLR-CCR or MPH-G-CCR natural, modified or recombinant sequence may be ligated to a heterologous sequence to encode a fusion protein. For example, for screening of peptide libraries for inhibitors of MMLR-CCR or MPH-G-CCR activity, it may be useful to encode a chimeric chemokine receptor protein expressing a
- 30 heterologous epitope that is recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between a chemokine receptor sequence and the heterologous protein sequence, so that the MMLR-CCR or MPH-G-CCR may be cleaved and purified away from the heterologous moiety.

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In an alternate embodiment of the invention, the coding sequence of MMLR-CCR or MPH-CCR could be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers MH et al (1980) Nuc Acids Res Symp Ser 215-23, Horn T et al (1980) Nuc Acids Res Symp Ser 225-32, etc). Alternatively, the protein itself could be produced using chemical methods to synthesize a MMLR-CCR or MPH-CCR amino acid sequence, in whole or in part. For example, peptides can be synthesized by solid phase techniques, cleaved from the resin, and purified by preparative high performance liquid chromatography (eg, Creighton (1983) Proteins Structures And Molecular Principles, WH Freeman and Co, New York NY). The composition of the synthetic peptides may be confirmed by amino acid analysis or sequencing (eg, the Edman degradation procedure; Creighton, supra)

Direct peptide synthesis can be performed using various solid-phase techniques (Roberge JY et al (1995) Science 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer) in accordance with the instructions provided by the manufacturer. Additionally, the amino acid sequence of MMLR-CCR or MPH-CCR, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequence from other α subunits, or any part thereof, to produce a variant polypeptide.

Identification of Transformants

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, its presence and expression should be confirmed. For example, if the MMLR-CCR or MPH-CCR is inserted within a marker gene sequence, recombinant cells containing MMLR-CCR or MPH-CCR can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a receptor sequence under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the receptor as well.

Alternatively, host cells which contain the coding sequence for MMLR-CCR or MPH-CCR and express MMLR-CCR or MPH-CCR may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridization and protein bioassay or immunoassay techniques which include membrane-based, solution-based, or chip-based technologies for the detection and/or quantification of the nucleic acid or protein.

The presence of the MMLR-CCR or MPH-CCR polynucleotide sequence can be detected by DNA-DNA or DNA-RNA hybridization or amplification using probes, portions or

fragments disclosed in SEQ ID NO:1 or SEQ ID NO:3, respectively. Nucleic acid amplification based assays involve the use of oligonucleotides or oligomers based on SEQ ID NO:1 or SEQ ID NO:3 to detect transformants containing MMLR-CCR or MPHG-CCR, respectively, DNA or RNA. As used herein "oligonucleotides" or "oligomers" refer to a nucleic acid sequence of at least about 10 nucleotides and as many as about 60 nucleotides, preferably about 15 to 30 nucleotides, and more preferably about 20-25 nucleotides which can be used as a probe or amplifier. Preferably, oligonucleotides are derived from the 3' region of the MMLR-CCR or MPHG-CCR nucleotide sequence shown in Figure 1A-D.

A variety of protocols for detecting and measuring the expression of the chemokine receptor polypeptides, using either polyclonal or monoclonal antibodies specific for the protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and fluorescent activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on the receptor polypeptides is preferred, but a competitive binding assay may be employed. These and other assays are described, among other places, in Hampton R et al (1990, Serological Methods, a Laboratory Manual, APS Press, St Paul MN) and Maddox DE et al (1983, J Exp Med 158:1211).

A wide variety of labels and conjugation techniques are known by those skilled in the art and can be used in various nucleic and amino acid assays. Means for producing labeled and can be used in various nucleic and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting MMLR-CCR or MPHG-CCR polynucleotide sequences include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the MMLR-CCR or MPHG-CCR sequence, or any portion of it, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3 or SP6 and labeled nucleotides.

A number of companies such as Pharmacia Biotech (Piscataway NJ), Promega (Madison WI), and US Biochemical Corp (Cleveland OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles and the like. Patents teaching the use of such labels include US Patents 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241. Also, recombinant immunoglobulins may be produced as shown in US Patent No. 4,816,567 and incorporated herein by reference.

Purification of Receptors

Host cells transformed with a MMLR-CCR or MPH-CCR nucleotide sequences may be cultured under conditions suitable for the expression and recovery of the encoded protein from cell culture. The protein produced by a recombinant cell may be secreted or may be contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing MMLR-CCR or MPH-CCR can be designed with signal sequences which directs secretion of MMLR-CCR or MPH-CCR through a particular prokaryotic or eukaryotic cell membrane. Other recombinant constructions may join MMLR-CCR or MPH-CCR to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins (Kroll DJ et al (1993) DNA Cell Biol 12:441-53; see also above discussion of vectors containing fusion proteins).

MMLR-CCR or MPH-CCR may also be expressed as a recombinant protein with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals (Porath J (1992) Protein Expr Purif 3:263-281), protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp, Seattle WA). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego CA) between the purification domain and MMLR-CCR or MPH-CCR is useful to facilitate purification.

Uses of The Receptors and Genetically Engineered Host Cells Containing the Receptors

The amino acid sequence of MMLR-CCR (SEQ ID NO:2) is shown in Figure 1A-D. Based upon its homology to MCP-1 CCR chemokine receptor, MCP-1RB (Chao, supra) particularly in the third transmembrane spanning domain which is known to be associated with G protein binding and its presence in a macrophage, 48 hour mixed lymphocyte reaction cDNA library and absence in a normal macrophage MMLR-CCR; and MMLR-CCR appears to be a chemokine receptor associated with leukocyte functioning. The amino acid sequence of MPH-CCR (SEQ ID NO:4) is shown in Figure 6A-C. Based upon its homology to C-C chemokine receptor 3 and MCP-1RA, and its presence in a macrophage library, MPH-CCR appears to be a chemokine receptor associated with leukocyte functioning.

Accordingly, the present invention provides MMLR-CCR and MPH-CCR amino acid sequences and genetically engineered host cells that express the receptors to evaluate, screen and identify the naturally occurring ligands, i.e., chemokines, in appropriate cellular supernatants.

The chemokine receptors of the present invention and genetically engineered host cells that express the receptors may also be used to identify substances, compounds or synthetic drugs that modulate receptor/ligand binding thereby modulating receptor activation and signalling transduction events. For example, such genetically engineered host cells could be used to screen peptide libraries or organic molecules capable of modulating MMLR-CCR activity.

In an embodiment of the present invention, MMLR-CCR, MPHG-CCR or a variant thereof and/or a cell line that expresses the MMLR-CCR, MPHG-CCR or variant thereof may be used to screen for antibodies, peptides, or other molecules, such as organic or inorganic molecules made by combinatorial chemistry, that act as modulators of monocyte/macrophage infiltration and chemotaxis, thereby identifying a therapeutic capable of modulating the immune response. Anti-receptor antibodies capable of neutralizing the activity of the receptor may be used to inhibit receptor activation, for example, in inflammatory diseases. Synthetic compounds, natural products, and other sources of potentially biologically active materials can be screened in a number of ways deemed to be routine to those of skill in the art. For example, nucleotide sequences encoding an extracellular domain of MMLR-CCR or MPHG-CCR may be expressed in a cell line which can be used for screening of modulators, either agonists or antagonists, of MMLR-CCR or MPHG-CCR activity, respectively. In one embodiment herein, an MMLR-CCR variant is one containing an isoleucine at residue position 121 instead of valine.

The ability of a test molecule to interfere with chemokine receptor activity or ligand binding may be determined by a measurement of monocyte chemotaxis (Falk et al 1980 J Immunol Methods 33:239). The activity of a chemokine receptor may also be monitored by measuring other responses such as Ca^{2+} flux (Grynkiewicz et al (1985) J Biol Chem 260:3440 and McColl et al (1993) J Immunol 150:4550-4555) and degranulation and respiratory burst responses (Zachariae et al 1990 J. Exp. Med. 171:2177-82) and regulation of adhesion molecule expression and cytokine production (Jiang et al 1992 J Immunol 148:2432-8).

Antibodies

Procedures well known in the art may be used for the production of antibodies to MMLR-CCR or MPHG-CCR polypeptides. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, Fab fragments and fragments produced by a Fab expression library. Neutralizing antibodies, i.e. those which inhibit biological activity of MMLR-CCR or MPHG-CCR polypeptides, are especially preferred for diagnostics and therapeutics.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, etc may be immunized by injection with MMLR-CCR or MPHG-CCR polypeptide or any portion.

fragment or oligopeptide which retains immunogenic properties. Depending on the host species, various adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol. BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are potentially useful human adjuvants which may be employed if purified MMLR-CCR polypeptide is administered to immunologically compromised individuals for the purpose of stimulating systemic defense.

Monoclonal antibodies to MMLR-CCR or MPHG-CCR polypeptide may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique originally described by Koehler and Milstein (1975, Nature 256:495-497), the human B-cell hybridoma technique (Kosbor et al (1983) Immunol Today 4:72; Cote et al (1983) Proc Natl Acad Sci 80:2026-2030) and the EBV-hybridoma technique (Cole et al (1985) Monoclonal Antibodies and Cancer Therapy, Alan R. Liss Inc, pp 77-96). In addition, techniques developed for the production of "chimeric antibodies", the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity can be used (Morrison et al (1984) Proc Natl Acad Sci 81:6851-6855; Neuberger et al (1984) Nature 312:604-608; Takeda et al (1985) Nature 314:452-454). Alternatively, techniques described for the production of single chain antibodies (US Patent No. 4,946,778) can be adapted to produce specific single chain antibodies.

Antibodies may also be produced by inducing *in vivo* production in the lymphocyte population or by screening recombinant immunoglobulin libraries or panels of highly specific binding reagents as disclosed in Orlandi et al (1989, Proc Natl Acad Sci 86: 3833-3837), and Winter G and Milstein C (1991; Nature 349:293-299).

Antibody fragments which contain specific binding sites for MMLR-CCR or MPHG-CCR may also be generated. For example, such fragments include, but are not limited to, the $F(ab')_2$ fragments which can be produced by pepsin digestion of the antibody molecule and the Fab fragments which can be generated by reducing the disulfide bridges of the $F(ab')_2$ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity (Huse WD et al (1989) Science 256:1275-1281).

MMLR-CCR- or MPHG-CCR-specific antibodies are useful for the diagnosis of

conditions and diseases associated with expression of MMLR-CCR or MPH-CCR polypeptide. A variety of protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the formation of a complex between a chemokine receptor and its specific antibody (or similar receptor-binding molecule) and the measurement of complex formation. A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies specific for two noninterfering epitopes on a specific MMLR-CCR or MPH-CCR protein is preferred, but a competitive binding assay may also be employed. These assays are described in Maddox DE et al (1983, J Exp Med 158:1211).

10 **Diagnostic Assays Using Receptor Specific Antibodies**

Anti-MMLR-CCR or MPH-CCR antibodies are useful for the diagnosis of conditions related to receptor activation, such as infection, inflammation, tumorigenesis, abnormal proliferation of cells and cardiovascular disease. Diagnostic assays for the chemokine receptors include methods utilizing the antibody and a label to detect a MMLR-CCR or MPH-CCR polypeptide in human body fluids, cells, tissues or sections or extracts of such tissues. The polypeptides and antibodies of the present invention may be used with or without modification. Frequently, the polypeptides and antibodies will be labeled by joining them, either covalently or noncovalently, with a reporter molecule. A wide variety of reporter molecules are known to those of skill in the art.

20 A variety of protocols for measuring a MMLR-CCR or MPH-CCR polypeptide, using either polyclonal or monoclonal antibodies specific for the respective protein are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and fluorescent activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a MMLR-CCR or MPH-CCR polypeptide is preferred, but a competitive binding assay may be employed. These assays are described, among other places, in Maddox, DE et al (1983, J Exp Med 158:1211).

25 In order to provide a basis for the diagnosis of disease, normal or standard values for MMLR-CCR or MPH-CCR polypeptide expression are established. This is accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with antibody to a MMLR-CCR or MPH-CCR polypeptide under conditions suitable for complex formation which are well known in the art. The amount of standard complex formation can be quantified by comparing it with a dilution series of positive controls where a known amount of antibody is combined with known concentrations of a purified MMLR-CCR or MPH-CCR

polypeptide. Then, standard values obtained from normal samples may be compared with values obtained from samples from subjects potentially affected by a disorder or disease related to a chemokine receptor polypeptide expression. Deviation between standard and subject values establishes the presence of the disease state.

5 Drug Screening

An MMLR-CCR polypeptide or MPH-CCR polypeptide, its immunogenic fragments or oligopeptides thereof can be used for screening therapeutic compounds in any of a variety of drug screening techniques. The fragment employed in such a test may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The abolition of activity or the
10 formation of binding complexes, between a receptor polypeptide and the agent being tested, may be measured. Accordingly, the present invention provides a method for screening a plurality of compounds for specific binding affinity with a MMLR-CCR, MPH-CCR or a fragment thereof, comprising providing a plurality of compounds; combining a chemokine receptor of the present invention or a fragment thereof with each of a plurality of compounds for a time sufficient to
15 allow binding under suitable conditions; and detecting binding of the chemokine receptor, or fragment thereof, to each of the plurality of compounds, thereby identifying the compounds which specifically bind the chemokine receptor. In such an assay, the plurality of compounds may be produced by combinatorial chemistry techniques known to those of skill in the art. In one embodiment of the present invention the MMLR-CCR or MPH-CCR oligopeptide is obtained
20 from an extracellular binding domain.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to a MMLR-CCR or MPH-CCR polypeptide and is described in detail in Geysen, European Patent Application 84/03564, published on September 13, 1984, incorporated herein by reference. In summary, large numbers of different small peptide
25 test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with MMLR-CCR or MPH-CCR fragments and washed. A bound chemokine receptor of the present invention is then detected by methods well known in the art. A purified MMLR-CCR or MPH-CCR can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing
30 antibodies can be used to capture the peptide and immobilize it on a solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding MMLR-CCR or MPH-CCR specifically compete with a test compound for binding MMLR-CCR or MPH-CCR. In this manner, the antibodies

can be used to detect the presence of any peptide which shares one or more antigenic determinants with MMLR-CCR or MPH-CCR, respectively.

Uses of Receptor Polynucleotide

An MMLR-CCR or MPH-CCR polynucleotide, or any part thereof, provides the basis for diagnostic and/or therapeutic compounds. For diagnostic purposes, MMLR-CCR or MPH-CCR polynucleotide sequences are used to detect and quantitate gene expression in conditions, disorders and diseases in which their activity may be implicated, for example, in infection, inflammation, tumorigenesis, proliferative disease and cardiovascular disease. For therapeutic purposes, MMLR-CCR or MPH-CCR antisense molecules are administered to individuals in conditions where it is desirable to down-regulate the presence of the receptor on the cell surface thereby inhibiting the activity of MMLR-CCR or MPH-CCR, respectively. Alternatively, for therapeutic purposes, sense polynucleotide sequences of MMLR-CCR or MPH-CCR are administered to individuals in conditions where it is desirable to enhance signal transduction events.

Included in the scope of the invention are oligonucleotide sequences, antisense RNA and DNA molecules and ribozymes, which function to destabilize MMLR-CCR or MPH-CCR mRNA or inhibit translation of a MMLR-CCR or MPH-CCR.

Another aspect of the subject invention is to provide for nucleic acid hybridization or PCR probes which can detect polynucleotide sequences, including genomic sequences, encoding mmlr-ccr or closely related molecules, such as alleles. The specificity of the probe, i.e. whether it is derived from a highly conserved, conserved or non-conserved region or domain, and the stringency of the hybridization or amplification (high, intermediate or low) determines whether the probe identifies only naturally occurring mmlr-ccr or related sequences. Probes for the detection of related nucleic acid sequences are selected from conserved or highly conserved nucleotide regions of known chemokine receptors, for example, the G protein binding domains. For the detection of identical nucleic acid sequences, or where maximum specificity is desired, such as in a diagnostic test, nucleic acid probes are selected from the non-conserved nucleotide regions or unique regions of mmlr-ccr polynucleotides. As used herein, the term "non-conserved nucleotide region" refers to a nucleotide region that is unique to the mmlr-ccr and mphg-ccr disclosed herein and does not occur in related chemokine receptors.

Diagnostic Uses of Receptor Polynucleotide

An MMLR-CCR or MPH-CCR encoding polynucleotide sequence is used for the diagnosis of diseases associated with receptor activation, such as infection, inflammation,

tumorigenesis, and cardiovascular disease. For example, polynucleotide sequences encoding MMLR-CCR or MPHG-CCR are used in hybridization or PCR assays of tissues from biopsies or autopsies or biological fluids, such as serum, synovial fluid or tumor biopsy, to detect abnormalities in MMLR-CCR or MPHG-CCR expression. Such qualitative or quantitative methods include Southern or northern analysis, dot blot or other membrane-based technologies; PCR technologies; dip stick, pin or chip technologies; and ELISA or other multiple sample format technologies. All of these techniques are well known in the art and are in fact the basis of many commercially available diagnostic kits.

Such assays are tailored to evaluate the efficacy of a particular therapeutic treatment regime and are used in animal studies, in clinical trials, or in monitoring the treatment of an individual patient. For disease diagnosis, a normal or standard profile for MMLR-CCR or MPHG-CCR expression is first established. This is accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with MMLR-CCR or MPHG-CCR or a portion thereof, under conditions suitable for hybridization or amplification. Standard hybridization is quantified by comparing the values obtained for normal subjects with a dilution series of positive controls run in the same experiment where a known amount of purified MMLR-CCR or MPHG-CCR is used. Standard values obtained from normal samples are compared with values obtained from samples from subjects potentially affected by a disorder or disease related to MMLR-CCR or MPHG-CCR expression. Deviation between standard and subject values establishes the presence of the disease state. If disease is established, an existing therapeutic agent is administered, and treatment profile or values may be generated. Finally, the assay may be repeated on a regular basis to evaluate whether the values progress toward or return to the normal or standard pattern. Successive treatment profiles may be used to show the efficacy of treatment over a period of several days or several months.

PCR as described in US Patent Nos. 4,683,195; 4,800,195; and 4,965,188 provides additional uses for oligonucleotides based upon the MMLR-CCR or MPHG-CCR sequence. Such oligomers are generally chemically synthesized, but they are generated enzymatically or produced from a recombinant source. Oligomers generally comprise two nucleotide sequences, one with sense orientation (5'→3') and one with antisense (3'←5') employed under optimized conditions for identification of a specific gene or condition. The same two oligomers, nested sets of oligomers, or even a degenerate pool of oligomers are employed under less stringent conditions for detection and/or quantitation of closely related DNA or RNA sequences.

Additionally methods to quantitate the expression of a particular molecule include

radiolabeling (Melby PC et al 1993 J Immunol Methods 159:235-44) or biotinylating (Duplaa C et.al 1993 Anal Biochem 229:36) nucleotides, coamplification of a control nucleic acid, and standard curves onto which the experimental results are interpolated. Quantitation of multiple samples is speeded up by running the assay in an ELISA format where the an oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

Therapeutic Uses of an MMLR-CCR or MPHG-CCR Polynucleotide

An MMLR-CCR or MPHG-CCR antisense molecule can provide the basis for treatment of various abnormal conditions related to receptor activation such as infection, inflammation, abnormal proliferation of cell, tumogenesis and cardiovascular disease, such as atherosclerosis, where it would be desirable to downregulate the presence of the receptor, thereby inhibiting MMLR-CCR or MPHG-CCR activity. Alternatively, polynucleotide sequences encoding MMLR-CCR or MPHG-CCR may provide the basis for gene therapy in the treatment of various abnormal conditions where it is desirable to up regulate the receptors thereby enhancing the immune response.

Expression vectors derived from retroviruses, adenovirus, herpes or vaccinia viruses, or from various bacterial plasmids, are used for delivery of recombinant MMLR-CCR or MPHG-CCR sense or antisense molecules to the targeted cell population. Methods which are well known to those skilled in the art can be used to construct recombinant vectors containing MMLR-CCR or MPHG-CCR related nucleotide sequences. Sec, for example, the techniques described in Maniatis et al (supra) and Ausubel et al (supra). Alternatively, recombinant MMLR-CCR or MPHG-CCR can be delivered to target cells in liposomes.

The full length cDNA sequence and/or its regulatory elements enable researchers to use a MMLR-CCR or MPHG-CCR as a tool in sense (Yousoufian H and HF Lodish 1993 Mol Cell Biol 13:98-104) or antisense (Eguchi et al (1991) Annu Rev Biochem 60:631-652) investigations of gene function. Oligonucleotides, designed from the cDNA or control sequences obtained from the genomic DNA can be used *in vitro* or *in vivo* to inhibit expression. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions.

Additionally, MMLR-CCR or MPHG-CCR expression can be modulated by transfecting a cell or tissue with expression vectors which express high levels of a MMLR-CCR or MPHG-CCR fragment in conditions where it would be preferable to inhibit MMLR-CCR or MPHG-CCR activity. Such constructs can flood cells with untranslatable sense or antisense sequences

which compete for binding with the naturally occurring receptor. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until all copies of the vector are disabled by endogenous nucleases. Such transient expression may last for a month or more with a non-replicating vector (Mettler I. personal communication) and even longer if appropriate replication elements are part of the vector system.

Modifications of gene expression can be obtained by designing antisense sequences to the control regions of the MMLR-CCR or MPH-CCR gene, such as the promoters, enhancers, and introns. Oligonucleotides derived from the transcription initiation site, eg, between -10 and +10 regions of the leader sequence, are preferred. Antisense RNA and DNA molecules may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes. Similarly, inhibition can be achieved using Hogeboom base-pairing methodology, also known as "triple helix" base pairing. Triple helix pairing compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. The mechanism of ribozyme action involves sequence specific hybridization of the ribozyme molecule to complementary target RNA, followed by an endonucleolytic cleavage. Within the scope of the invention are engineered hammerhead motif ribozyme molecules that specifically and efficiently catalyze endonucleolytic cleavage of MMLR-CCR or MPH-CCR RNA sequences.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites which include the following sequences, GUA, GUU and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides corresponding to the region of the target gene containing the cleavage site may be evaluated for secondary structural features which may render the oligonucleotide sequence inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.

Both antisense RNA and DNA molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of RNA molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding the antisense RNA molecule. Such DNA sequences may be incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, antisense cDNA constructs that synthesize antisense RNA

constitutively or inducibly can be introduced into cell lines, cells or tissues.

DNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences of the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule.

Methods for introducing vectors into cells or tissue include those methods discussed infra. In addition, several of these transformation or transfection methods are equally suitable for ex vivo therapy.

Furthermore, the MMLR-CCR or MPHG-CCR polynucleotide sequences disclosed herein may be used in molecular biology techniques that have not yet been developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including but not limited to such properties as the triplet genetic code and specific base pair interactions.

Detection and Mapping of Polynucleotide Sequences Related to MMLR-CCR OR MPHG-CCR

The nucleic acid sequence for MMLR-CCR or MPHG-CCR can also be used to generate hybridization probes as previously described, for mapping the endogenous genomic sequence. The sequence may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. These include in situ hybridization to chromosomal spreads (Verma et al (1988) Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York City), flow-sorted chromosomal preparations, or artificial chromosome constructions such as YACs, bacterial artificial chromosomes (BACs), bacterial P1 constructions or single chromosome cDNA libraries.

In situ hybridization of chromosomal preparations and physical mapping techniques such as linkage analysis using established chromosomal markers are invaluable in extending genetic maps. Examples of genetic maps can be found in Science (1995; 270:410f and 1994; 265:1981f). Often the placement of a gene on the chromosome of another mammalian species may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms, or parts thereof, by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome, such as ataxia telangiectasia (AT), has been crudely localized by genetic linkage to a particular genomic region, for example, AT to 11q22-23 (Gatti et al (1988) Nature 336:577-580), any additional sequences mapping to that area may represent associated or regulatory genes for further investigation. The

nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc between normal, carrier or affected individuals.

Pharmaceutical Compositions

5 The present invention relates to pharmaceutical compositions which may comprise nucleotides, proteins, antibodies, antagonists, or inhibitors, or agonists of MMLR-CCR or MPHIG-CCR alone or in combination with at least one other agent, such as stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier, including, but not limited to, saline, buffered saline, dextrose, and water. Any of these molecules can be
10 administered to a patient alone, or in combination with other agents, drugs or hormones, in pharmaceutical compositions where it is mixed with excipient(s) or pharmaceutically acceptable carriers. In one embodiment of the present invention, the pharmaceutically acceptable carrier is pharmaceutically inert.

Administration of Pharmaceutical Compositions

15 Administration of pharmaceutical compositions is accomplished orally or parenterally. Methods of parenteral delivery include topical, intra-arterial (directly to the tumor), intramuscular, subcutaneous, intramedullary, intrathecal, intraventricular, intravenous, intraperitoneal, or intranasal administration. In addition to the active ingredients, these
20 pharmaceutical compositions may contain suitable pharmaceutically acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of "Remington's Pharmaceutical Sciences" (Maack Publishing Co, Easton PA).

 Pharmaceutical compositions for oral administration can be formulated using
25 pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions and the like, for ingestion by the patient.

 Pharmaceutical preparations for oral use can be obtained through combination of active
30 compounds with solid excipient, optionally grinding a resulting mixture, and processing the mixture of granules, after adding suitable auxiliaries, if desired, to obtain tablets or dragee cores. Suitable excipients are carbohydrate or protein fillers such as sugars, including lactose, sucrose, mannitol, or sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose such as

methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; and gums including arabic and tragacanth; and proteins such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, alginic acid, or a salt thereof, such as sodium alginate.

5 Dragee cores are provided with suitable coatings such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, ie, dosage.

10 Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating such as glycerol or sorbitol. Push-fit capsules can contain active ingredients mixed with a filler or binders such as lactose or starches, lubricants such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty

15 oils, liquid paraffin, or liquid polyethylene glycol with or without stabilizers. Pharmaceutical formulations for parenteral administration include aqueous solutions of active compounds. For injection, the pharmaceutical compositions of the invention may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks's solution, Ringer's solution, or physiologically buffered saline. Aqueous injection

20 suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include fatty oils such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate or triglycerides, or liposomes. Optionally, the suspension may also contain suitable

25 stabilizers or agents which increase the solubility of the compounds to allow for the preparation of highly concentrated solutions.

For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.

Manufacture and Storage

30 The pharmaceutical compositions of the present invention may be manufactured in a manner that known in the art, eg, by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping or lyophilizing processes.

The pharmaceutical composition may be provided as a salt and can be formed with many

acids, including but not limited to hydrochloric, sulfuric, acetic, lactic, tartaric, malic, succinic, etc. Salts tend to be more soluble in aqueous or other protonic solvents that are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder in 1mM-50mM histidine, 0.1%-2% sucrose, 2%-7% mannitol at a pH range of 4.5 to 5.5 that is combined with buffer prior to use.

After pharmaceutical compositions comprising a compound of the invention formulated in a acceptable carrier have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of HCAP, such labeling would include amount, frequency and method of administration.

Therapeutically Effective Dose

Pharmaceutical compositions suitable for use in the present invention include compositions wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays, eg, of neoplastic cells, or in animal models, usually mice, rabbits, dogs, or pigs. The animal model is also used to achieve a desirable concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of protein or its antibodies, antagonists, or inhibitors or agonists which ameliorate the symptoms or condition. Therapeutic efficacy and toxicity of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, eg, ED50 (the dose therapeutically effective in 50% of the population) and LD50 (the dose lethal to 50% of the population). The dose ratio between therapeutic and toxic effects is the therapeutic index, and it can be expressed as the ratio, ED50/LD50. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies is used in formulating a range of dosage for human use. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED50 with little or no toxicity. The dosage varies within this range depending upon the dosage form employed, sensitivity of the patient, and the route of administration.

The exact dosage is chosen by the individual physician in view of the patient to be treated. Dosage and administration are adjusted to provide sufficient levels of the active moiety

or to maintain the desired effect. Additional factors which may be taken into account include the severity of the disease state, eg, tumor size and location; age, weight and gender of the patient; diet, time and frequency of administration, drug combination(s), reaction sensitivities, and tolerance/response to therapy. Long acting pharmaceutical compositions might be administered every 3 to 4 days, every week, or once every two weeks depending on half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from 0.1 to 100,000 micrograms, up to a total dose of about 1 g, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature. See US Patent Nos. 4,657,760; 5,206,344; or 5,225,212. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions or locations, for example.

It is contemplated that antagonists or agonists of MMLR-CCR or MPHG-CCR HCAP can be delivered in a suitable formulation to individuals having conditions where it is desirable to inhibit or enhance, respectively, chemokine receptor activity.

These examples are provided by way of illustration and are not included for the purpose of limiting the invention.

INDUSTRIAL APPLICABILITY

I CONSTRUCTION OF MMLR-CCR LIBRARY AND ISOLATION OF cDNA

CLONES

By way of example, construction of the MMLR2DT01 cDNA library is described. The MPHGN0T03 library was constructed using similar methodology.

The normal peripheral blood macrophages used for this library were obtained from two 24-year-old, Caucasian males. This library represents a mixture of allogeneically stimulated human macrophage populations obtained from Ficoll/Hypaque purified buffy coats. The cells from the two different donors (not typed for HLA alleles) were incubated at a density of 1×10^6 /ml and cultured for 48 hours in DME containing 10% human serum.

After incubation, macrophages mostly adhered to the plastic surface of the petri dish, whereas most other cell types, B and T lymphocytes, remained in solution. The DME was decanted from the wells, and the wells were washed with phosphate buffered saline (PBS). Macrophages were released from the plastic surface by gently scraping the petri dishes in PBS/1 mM EDTA. Macrophages were lysed immediately in buffer containing guanidinium isothiocyanate.

The lysate was extracted twice with a mixture of phenol and chloroform, pH 8.0 and centrifuged over a CsCl cushion using an Beckman SW28 rotor in a L8-70M Ultracentrifuge (Beckman Instruments). The RNA was precipitated using 0.3 M sodium acetate and 2.5 volumes of ethanol, resuspended in water and DNase treated for 15 min at 37°C. The total RNA was isolated using the Qiagen Oligotex kit (QIAGEN Inc, Chatsworth CA). It must be noted that some contaminating T and B lymphocytes may also have been present.

The poly A⁺ RNA was used in the SuperScript Plasmid System for cDNA Synthesis and Plasmid Cloning (catalogue #18248-013; Gibco BRL, Gaithersburg MD) with the recommended protocol. cDNAs were fractionated on a Sepharose CL4B column (catalog #275105, Pharmacia, and those cDNAs exceeding 400 bp were ligated into pSport I. The plasmid was transformed into chemically competent DH5 host cells (Gibco BRL).

Plasmid DNA was released from the cells and purified using the Miniprep Kit (Catalogue # 77468; Advanced Genetic Technologies Corporation, Gaithersburg MD). This kit consists of a 96 well block with reagents for 960 purifications. The recommended protocol was employed except for the following changes: 1) the 96 wells were each filled with only 1 ml of sterile Terrific Broth (Catalog # 22711, Gibco/BRL, Gaithersburg MD) with carbenicillin at 25 mg/L and glycerol at 0.4%; 2) the bacteria were cultured for 24 hours after the wells were inoculated and then lysed with 60 µl of lysis buffer; 3) a centrifugation step employing the Beckman GS-6R @2900 rpm for 5 min was performed before the contents of the block were added to the primary filter plate; and 4) the optional step of adding isopropanol to TRIS buffer was not routinely performed. After the last step in the protocol, samples were transferred to a Beckman 96-well block for storage.

Alternative methods of purifying plasmid DNA include the use of MAGIC MINIPREPS™ DNA Purification System (Catalogue #A7100, Promega, Madison WI) or QIAwell™-s Plasmid, QIAwell PLUS DNA and QIAwell ULTRA DNA Purification Systems (QIAGEN® Chatsworth CA).

The cDNAs were sequenced by the method of Sanger F and AR Coulson (1975; J Mol Biol 94:441f), using a Hamilton Micro Lab 2200 (Hamilton, Reno NV) in combination with four Peltier Thermal Cyclers (PTC200 from MJ Research, Watertown MA) and Applied Biosystems 377 or 373 DNA Sequencing Systems (Perkin Elmer) and reading frame was determined.

II Homology Searching of cDNA Clones and Their Deduced Proteins

Each cDNA was compared to sequences in GenBank using a BLAST search (Basic Local Alignment Search Tool; Altschul SF (1993) J. Mol. Evol. 36: 290-300; Altschul SF et al (1990)

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J. Mol. Biol. 215:403-410). This method identified Incyte Clone 478861 as a non-exact match to human MCP-1RB receptor (NCBI GI 472558) Charo (supra) and Incyte Clone 442279 as being a non-exact match to C-C chemokine receptor 3 and MCP-1RA (Charo, supra).

BLAST was used to search for local sequence alignments. BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches and in identifying homologs. BLAST is useful for matches which do not contain gaps. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP).

An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user. The BLAST approach is to look for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output.

III DETERMINATION OF READING FRAME OF cDNA CLONE

The reading frame of individual cDNA clones obtained from the MMLR2DT01 library was obtained by analyzing the polynucleotide sequences for the presence of start (ATG, GTG, etc.) and stop codons (TGA, TAA, TAG). Typically, one frame will continue throughout the major portion of all of a cDNA sequence and the other two pending frames tend to contain numerous stop codons. Algorithms for determining reading frame have been developed which analyze the occurrence of individual nucleotide bases of each putative codon triplet (e.g., Fickett, J.W. (1982) Nucleic Acids Research 10:5303). Coding DNA tends to contain predominantly certain nucleotides within certain triplet periodicities, such as a significant preference for pyrimidines in the third codon position. These algorithms have been incorporated into widely available software and are used to determine coding potential (and frame) of a given stretch of DNA. This algorithm-derived information, combined with start/stop codon information, was used to determine proper frame of individual clones within the library with a high degree of certainty, thus permitting the correct reading frame alignment with appropriate expression vehicles.

IV Extension of MMLR-CCR OR MPHG-CCR to Recover Regulatory Elements

The nucleic acid sequence of MMLR-CCR or MPHG-CCR is used to design oligonucleotide primers for obtaining full length sequences from genomic libraries. One primer is synthesized to initiate extension in the antisense direction (XLR) and the other is synthesized to extend sequence in the sense direction (XLF). The primers allow the known MMLR-CCR or MPHG-CCR sequence to be extended "outward" generating amplicons containing new, unknown nucleotide sequence for the control region of interest. The initial primers are designed from the cDNA using Oligo 4.0 (National Biosciences Inc, Plymouth MN), or another appropriate program, to be 22-30 nucleotides in length, to have a GC content of 50% or more, and to anneal to the target sequence at temperatures about 68°-72° C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations is avoided.

A human genomic library is used to extend and amplify 5' upstream sequence. If necessary, a second set of primers is designed to further extend the known region. By following the instructions for the XL-PCR kit (Perkin Elmer) and thoroughly mixing the enzyme and reaction mix, high fidelity amplification is obtained. Beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, PCR is performed using the Peltier Thermal Cycler (PTC200; MJ Research, Watertown MA) and the following parameters:

Step 1	94° C for 1 min (initial denaturation)
Step 2	65° C for 1 min
Step 3	68° C for 6 min
Step 4	94° C for 15 sec
Step 5	65° C for 1 min
Step 6	68° C for 7 min
Step 7	Repeat step 4-6 for 15 additional cycles
Step 8	94° C for 15 sec
Step 9	65° C for 1 min
Step 10	68° C for 7:15 min
Step 11	Repeat step 8-10 for 12 cycles
Step 12	72° C for 8 min
Step 13	4° C (and holding)

A 5-10 μ l aliquot of the reaction mixture is analyzed by electrophoresis on a low concentration (about 0.6-0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. The largest products or bands are selected and cut out of the gel.

Further purification involves using a commercial gel extraction method such as QIAQuick™ (QIAGEN Inc). After recovery of the DNA, Klenow enzyme is used to trim single-stranded, nucleotide overhangs creating blunt ends which facilitate religation and cloning.

After ethanol precipitation, the products are redissolved in 13 μ l of ligation buffer, 1 μ l

T4-DNA ligase (15 units) and 1 μ l T4 polynucleotide kinase are added, and the mixture is incubated at room temperature for 2-3 hours or overnight at 16° C. Competent *E. coli* cells (in 40 μ l of appropriate media) are transformed with 3 μ l of ligation mixture and cultured in 80 μ l of SOC medium (Sambrook J et al, supra). After incubation for one hour at 37° C, the whole transformation mixture is plated on Luria Bertani (LB)-agar (Sambrook J et al, supra) containing 2x Carb. The following day, several colonies are randomly picked from each plate and cultured in 150 μ l of liquid LB/2xCarb medium placed in an individual well of an appropriate, commercially-available, sterile 96-well microtiter plate. The following day, 5 μ l of each overnight culture is transferred into a non-sterile 96-well plate and after dilution 1:10 with water, 5 μ l of each sample is transferred into a PCR array.

For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer and one or both of the gene specific primers used for the extension reaction are added to each well. Amplification is performed using the following conditions:

- | | | |
|----|--------|--|
| 15 | Step 1 | 94° C for 60 sec |
| | Step 2 | 94° C for 20 sec |
| | Step 3 | 55° C for 30 sec |
| | Step 4 | 72° C for 90 sec |
| | Step 5 | Repeat steps 2-4 for an additional 29 cycles |
| 20 | Step 6 | 72° C for 180 sec |
| | Step 7 | 4° C (and holding) |

Aliquots of the PCR reactions are run on agarose gels together with molecular weight markers. The sizes of the PCR products are compared to the original partial cDNAs, and appropriate clones are selected, ligated into plasmid and sequenced.

V Labeling of Hybridization Probes

Hybridization probes derived from SEQ ID NO:1 or SEQ ID NO:3 are employed to screen cDNAs, mRNAs or genomic DNAs. Although the labeling of oligonucleotides, consisting of about 20 base-pairs, is specifically described, essentially the same procedure is used with larger cDNA fragments. Oligonucleotides are labeled by combining 50 pmol of each oligomer and 250 mCi of [γ -³²P] adenosine triphosphate (Amersham, Chicago IL) and T4 polynucleotide kinase (DuPont NEN®, Boston MA). The labeled oligonucleotides are purified with Sephadex G-25 super fine resin column (Pharmacia). A portion containing 10⁷ counts per minute of each is used in a typical membrane based hybridization analysis of human genomic DNA digested with one of the following endonucleases (Asc I, Bgl II, EcoR I, Pst I, Xba I, or

Pvu II; DuPont NEN®).

The DNA from each digest is fractionated on a 0.7 percent agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. After XOMAT AR™ film (Kodak, Rochester NY) is exposed to the blots in a Phosphorimager cassette (Molecular Dynamics, Sunnyvale CA) for several hours, hybridization patterns are compared visually.

VI Antisense Molecules

The MMLR-CCR or MPH-CCR sequence, or any part thereof, is used to inhibit *in vivo* or *in vitro* expression of endogenous MMLR-CCR or MPH-CCR, respectively. Although use of antisense oligonucleotides, consisting of about 20 base-pairs, is specifically described, essentially the same procedure is used with larger cDNA fragments. An oligonucleotide based on the coding sequence of MMLR-CCR or MPH-CCR is used to inhibit expression of endogenous MMLR-CCR or MPH-CCR. Using Oligo 4.0, the complementary oligonucleotide is designed from the conserved 5' sequence and used to inhibit either transcription, by preventing promoter binding to the upstream nontranslated sequence, or translation of an MMLR-CCR or MPH-CCR transcript by preventing the ribosome from binding to the mRNA.

VII Production of MMLR-CCR OR MPH-CCR Specific Antibodies

For production of polyclonal antibodies, the deduced amino acid sequence of MMLR-CCR or MPH-CCR is analyzed using DNASTAR software (DNASTAR Inc) to determine regions of high immunogenicity and a corresponding oligopeptide is synthesized and used to raise antibodies in rabbits. Analysis to select appropriate epitopes, such as those near the C-terminus or in adjacent hydrophilic regions is described by Ausubel FM et al (supra). An oligopeptide of about 15 residues in length is synthesized using an ABI Peptide Synthesizer Model 431A (Perkin Elmer, Norwalk, CN) using fmoc-chemistry, and coupled to keyhole limpet hemocyanin (KLH, Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS; Ausubel FM et al, supra). Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity, for example, by binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radioiodinated, goat anti-rabbit IgG.

VIII Purification of MMLR-CCR Or MPH-CCR Using Specific Antibodies

Endogenous or recombinant MMLR-CCR or MPH-CCR can be purified by

immunoaffinity chromatography using antibodies specific for MMLR-CCR or MPHG-CCR. An immunoaffinity column is constructed by covalently coupling MMLR-CCR or MPHG-CCR antibody to an activated chromatographic resin such as CNBr-activated Sepharose (Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing MMLR-CCR or MPHG-CCR is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of MMLR-CCR or MPHG-CCR (eg. high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/MMLR-CCR or MPHG-CCR binding (eg, a buffer of pH 2-3 or a high concentration of a chaotrope such as urea or thiocyanate ion), and MMLR-CCR or MPHG-CCR is collected.

IX Identification of Molecules Which Interact with MMLR-CCR Or MPHG-CCR

MMLR-CCR or MPHG-CCR, or a biologically active fragment thereof, is labeled with ¹²⁵I Bolton-Hunter reagent (Bolton, AE and Hunter, WM (1973) Biochem J 133: 529). Candidate small molecules previously arrayed in the wells of a 96 well plate are incubated with the labeled MMLR-CCR or MPHG-CCR, washed and any wells with labeled MMLR-CCR or MPHG-CCR complex are assayed. Data obtained using different concentrations of MMLR-CCR or MPHG-CCR are used to calculate values for the number, affinity, and association of MMLR-CCR or MPHG-CCR with the candidate molecules.

20 X Northern Analysis

Northern analysis of various tissues obtained from Clontech Labs using the 0.6kb SalI/NotI fragment from Incyte Clone 478861, which encodes MMLR-CCR, was performed using .2X SSC / .1% SDS washes. The results showed that a 4.0 kb major transcript exists in all of the 16 tissues represented, see Figure 5, which include normal heart, brain, placenta, lung, liver skeletal muscle, kidney, pancreas, spleen, thymus, prostate, testis, ovary, small intestine, colon and leukocyte. As illustrated in Figure 5, the transcript was most abundant in lung, spleen, thymus, ovary, small intestine and peripheral blood leukocyte preparations. A smaller transcript at 2.5 kb is observed in placenta.

All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited

to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: INCYTE PHARMACEUTICALS, INC.
- (ii) TITLE OF THE INVENTION: NOVEL CHEMOKINE RECEPTORS
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) PCT APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/638,081
 - (B) FILING DATE: 26-APR-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0060 PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1557 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: chemokine
 - (B) CLONE: 478861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAACAAGATG GATTATCAAG TGCTAAGTCC AATCTATGAC ATCAATTATT ATATATCGGA 60
CCCCTGCCAA AAAAATCAAT GTGAAGCAA TCGCAGCCCG CCTCTGCCT CCGCTCTACT 120

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CACTGGTGTT CATCTTTGGT TTTGTGGGCA ACATGCTGGT CATCTCATC CTGATAAACT 180
GCAAAAAGGCT GAAGAGCATG ACTGACATCT ACCTGCTCAA CCGTGGCATC TCTGACCTGT 240
TTTTCTTTCT TACTGTCCCC TTCTGGGCTC ACTATGCTGC CGCCAGTGG GACTTTGGAA 300
ATACAATGTG TCAACTCTTG ACAGGGTCTT ATTTATAGG CTCTTCTCT GGAATCTTCT 360
TCATCATCCT CCGTACAATC GGGGTGGTGA CAAGTGTGAT CACTGGGTG GTGGCTGTGT 420
AAGCCAGGAG GGTCACTTTT CCAGGAATC ATCTTTACCA GATCTCAAAA AGAAGGTCTT CATTAACCT 480
TTGGCTCTCT CCGAGCTTCA TTTTCATACA TTAAGATAG TCATCTTGGG GCTGGTCTCT CCGTCTCTT 540
GCAGCTTCAT TCTGCTACTG GGAATCCTAA AAACCTCTGT TCGGTGTGCG AATGAGAAGA 600
TCATGGTCAT CTGCTACTCG CTTATCTTCA CCACTCTGAT TGTATTATTT CTCTCTCTGG 660
AGAGGCCAGG GGTGTGAGG CTTATCTTCA CCACTCTGAT TGTATTATTT CTCTCTCTGG 720
CTCCCTACAA CATTTGCTCT CTCTCTGAACA CCATCATGAT TGTATTATTT CTCTCTCTGG 780
AGAGGCCAGG GGTGTGAGG CTTATCTTCA CCACTCTGAT TGTATTATTT CTCTCTCTGG 840
CGAGTAGCTC TAACAGGTTG GACCAAGCTA TGCAGGTGAC AGAGACTCTT GGGATGACGC 900
ACTGCTGCAT CAACCCCATC ATCTATGCCT TTGCTGGGGA GAAGTTCAGA AACTACTCTCT 960
TAGTCTTCTT CCAAAAGCAC ATTGCCAAAC GCTTCTGCAA ATGCTGTCTT ATTTTCCAGC 1020
AAGAGGCTCC CGAGCCAGCA AGCTCAGTTT ACACCCGATC CACTGGGGAG CAGGAAATAT 1080
CTGTGGGCTT TGACACGGA CTCAGTGGG CTGGTGACCC AGCTAGAGT TTAAGAAGAA 1140
TTTAGTTTTT ATACACAGCC TGGGCTGGGG CTGGGGTGGG AGAGTCTTTT TTAAGAAGAA 1200
GTTACTGTTA TAGAGGGTCT AAGATTATC CATTATTGTC GCATCTGTTT AAAGTAGATT 1260
AGATCTTTTA AGCCCATCAA TTAGAGAAAG CCAAAATCAA ATATGTTGAT GAAAATAGG 1320
AACCTTTTTA TCTCCCTTCT ACATGTCATCA AGTTATTGAC AAATCTCTCC TTCACTCGGA 1380
AAGTTTCTTA TCTCCCTTCT ACATGTCATCA AGTTATTGAC AAATCTCTCC TTCACTCGGA 1440
ATCTGAACAG AATACACAAA ATATTTCAG AAATGTACAA CTTTTTACTT AGTACAGGC 1500
AACATATAGG TTGTAATGT GTTTAAACA GGTCTTTGTC TGCATGCGG GACAAAAGAC 1557
ATGAATATGA TTAGTAAGA AACGACACTT TTCATGTGTC AAAAAA AAAA

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(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: chemokine
 - (B) CLONE: 478861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Thr Ser Ile Ile Ile Tyr Arg Ser Pro Ala Lys Lys Ile Asn Val
1 5 10 15
Lys Gln Ile Ala Ala Arg Leu Leu Pro Pro Leu Tyr Ser Leu Val Phe
20 25 30
Ile Phe Gly Phe Val Gly Asn Met Leu Val Ile Leu Ile Leu Asn
35 40 45
Cys Lys Arg Leu Lys Ser Met Thr Asp Ile Tyr Leu Leu Asn Leu Ala
50 55 60
Ile Ser Asp Leu Phe Phe Leu Leu Thr Val Pro Phe Trp Ala His Tyr
65 70 75 80
Ala Ala Ala Gln Trp Asp Phe Gly Asn Thr Met Cys Gln Leu Leu Thr
85 90 95
Gly Leu Tyr Phe Ile Gly Phe Phe Ser Gly Ile Phe Phe Ile Ile Leu
100 105 110
Leu Thr Ile Asp Arg Tyr Leu Ala Val Val His Ala Val Phe Ala Leu
115 120 125
Lys Ala Arg Thr Val Thr Phe Gly Val Val Thr Ser Val Ile Thr Trp
130 135 140

```


Val Val Ala Val Phe Ala Ser Leu Pro Gly Ile Ile Phe Thr Arg Ser
 145 150 155 160
 Gln Lys Glu Gly Leu His Tyr Thr Cys Ser Ser His Phe His Thr Leu
 165 170 175
 Lys Ile Val Ile Leu Gly Leu Val Leu Pro Leu Leu Val Met Val Ile
 180 185 190
 Cys Tyr Ser Gly Ile Leu Lys Thr Leu Arg Cys Arg Asn Glu Lys
 195 200 205
 Lys Arg His Arg Ala Val Arg Leu Ile Phe Thr Ile Met Ile Val Tyr
 210 215 220
 Phe Leu Phe Trp Ala Pro Tyr Asn Ile Val Leu Leu Leu Asn Thr Phe
 225 230 235 240
 Gln Glu Phe Phe Gly Leu Asn Asn Cys Ser Ser Ser Asn Arg Leu Asp
 245 250 255
 Gln Ala Met Gln Val Thr Glu Thr Leu Gly Met Thr His Cys Cys Ile
 260 265 270
 Asn Pro Ile Ile Tyr Ala Phe Val Gly Glu Lys Phe Arg Asn Tyr Leu
 275 280 285
 Leu Val Phe Phe Gln Lys His Ile Ala Lys Arg Phe Cys Lys Cys Cys
 290 295 300
 Ser Ile Phe Gln Gln Glu Ala Pro Glu Arg Ala Ser Ser Val Tyr Thr
 305 310 315 320
 Arg Ser Thr Gly Glu Gln Glu Ile Ser Val Gly Leu
 325 330

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: chemokine
 (B) CLONE: 442279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676	677	678	679	680	681	682	683	684	685	686	687	688	689	690	691	692	693	694	695	696	697	698	699	700	701	702	703	704	705	706	707	708	709	710	711	712	713	714	715	716	717	718	719	720	721	722	723	724	725	726	727	728	729	730	731	732	733	734	735	736	737	738	739	740	741	742	743	744	745	746	747	748	749	750	751	752	753	754	755	756	757	758	759	760	761	762	763	764	765	766	767	768	769	770	771	772	773	774	775	776	777	778	779	780	781	782	783	784	785	786	787	788	789	790	791	792	793	794	795	796	797	798	799	800	801	802	803	804	805	806	807	808	809	810	811	812	813	814	815	816	817	818	819	820	821	822	823	824	825	826	827	828	829	830	831	832	833	834	835	836	837	838	839	840	841	842	843	844	845	846	847	848	849	850	851	852	853	854	855	856	857	858	859	860	861	862	863	864	865	866	867	868	869	870	871	872	873	874	875	876	877	878	879	880	881	882	883	884	885	886	887	888	889	890	891	892	893	894	895	896	897	898	899	900	901	902	903	904	905	906	907	908	909	910	911	912	913	914	915	916	917	918	919	920	921	922	923	924	925	926	927	928	929	930	931	932	933	934	935	936	937	938	939	940	941	942	943	944	945	946	947	948	949	950	951	952	953	954	955	956	957	958	959	960	961	962	963	964	965	966	967	968	969	970	971	972	973	974	975	976	977	978	979	980	981	982	983	984	985	986	987	988	989	990	991	992	993	994	995	996	997	998	999	1000
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*GTGTTACAT	CACTAAACTC	ATCGCCACCA	CCCCTGCTG	CATCAACCTT	CTCCTGTATG	1080
CGTTTCTTGA	TGGGACATTT	AGCAAAATACC	TCTGCCGCTG	TTTCCATCTG	CGTAGTAACA	1140
CCCCACTTCA	ACCCAGGGGG	CAGTCTGCAC	AAGGCACATC	GAGGGAAGAA	CCTGACCATT	1200
CCACCGAAGT	GTAAACTAGC	ATCCACCAAA	TGCAAGAAGA	ATAACATGG	ATTTTCATCT	1260
TTCTGCATTA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA	1316

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: chemokine
- (B) CLONE: 442279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Asn	Tyr	Thr	Leu	Ala	Pro	Glu	Asp	Glu	Tyr	Asp	Val	Leu	Ile
1									5						
Glu	Gly	Glu	Leu	Glu	Ser	Asp	Glu	Ala	Glu	Gln	Cys	Asp	Lys	Tyr	Asp
									10						
Ala	Gln	Ala	Leu	Ser	Ala	Gln	Leu	Val	Pro	Ser	Leu	Cys	Ser	Ala	Val
									20						
Phe	Val	Ile	Gly	Val	Leu	Asp	Asn	Leu	Leu	Val	Val	Leu	Ile	Leu	Val
									30						
Lys	Tyr	Lys	Gly	Leu	Lys	Arg	Val	Glu	Asn	Ile	Tyr	Leu	Leu	Asn	Leu
									40						
Ala	Val	Ser	Asn	Leu	Cys	Phe	Leu	Leu	Thr	Leu	Pro	Phe	Trp	Ala	His
									50						
Ala	Gly	Gly	Asp	Pro	Met	Cys	Lys	Ile	Leu	Ile	Gly	Leu	Tyr	Xaa	Leu
									60						
Gly	Leu	Tyr	Ser	Glu	Thr	Xaa	Phe	Asn	Cys	Leu	Leu	Thr	Val	Gln	Arg
									70						
Tyr	Leu	Val	Phe	Leu	His	Lys	Gly	Asn	Phe	Phe	Ser	Ala	Arg	Arg	
									80						
Val	Pro	Cys	Gly	Ile	Ile	Thr	Ser	Val	Leu	Ala	Trp	Val	Thr	Ala	Ile
									90						
Leu	Ala	Thr	Leu	Pro	Glu	Tyr	Val	Val	Tyr	Lys	Pro	Gln	Met	Glu	Asp
									100						
Gln	Lys	Tyr	Lys	Cys	Ala	Phe	Ser	Arg	Thr	Pro	Phe	Leu	Pro	Ala	Asp
									110						
Glu	Thr	Phe	Trp	Lys	His	Phe	Leu	Thr	Leu	Lys	Met	Asn	Ile	Ser	Val
									120						
Leu	Val	Leu	Pro	Leu	Phe	Ile	Phe	Thr	Phe	Leu	Tyr	Val	Gln	Met	Arg
									130						
Lys	Thr	Leu	Arg	Phe	Arg	Glu	Gln	Arg	Tyr	Ser	Leu	Phe	Lys	Leu	Val
									140						
Phe	Ala	Ile	Met	Val	Val	Phe	Leu	Leu	Met	Trp	Ala	Pro	Tyr	Asn	Ile
									150						
Ala	Phe	Phe	Leu	Ser	Thr	Phe	Lys	Glu	His	Phe	Ser	Leu	Ser	Asp	Cys
									160						
Lys	Ser	Ser	Tyr	Asn	Leu	Asp	Lys	Ser	Val	His	Ile	Thr	Lys	Leu	Ile
									170						
Ala	Thr	Thr	His	Cys	Cys	Ile	Asn	Pro	Leu	Leu	Tyr	Ala	Phe	Leu	Asp
									180						

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Gly	Thr	Phe	Ser	Lys	Tyr	Leu	Cys	Arg	Cys	Phe	His	Leu	Arg	Ser	Asn	
					310					315					320	
305																
Thr	Pro	Leu	Gln	Pro	Arg	Gly	Gln	Ser	Ala	Gln	Gly	Thr	Ser	Arg	Glu	
				325					330					335		
Glu	Pro	Asp	His	Ser	Thr	Glu	Val									
			340													

CLAIMS

1. A purified polynucleotide comprising a nucleic acid sequence encoding the polypeptide having the sequence as depicted in SEQ ID NO:2.
- 5 2. The polynucleotide of Claim 1 wherein the polynucleotide sequence comprises SEQ ID NO:1.
3. The purified polynucleotide of Claim 1 wherein said polypeptide has isoleucine at residue 121.
4. An antisense molecule comprising the complement of the polynucleotide of Claim 2 or a
10 portion thereof.
5. An expression vector comprising the polynucleotide of Claim 1.
6. A host cell transformed with the expression vector of Claim 5.
7. A diagnostic composition for the detection of mmlr-ccr polynucleotide sequences comprising the polynucleotide of Claim 1, or a fragment thereof.
- 15 8. A purified polypeptide comprising the amino acid sequence as depicted in SEQ ID NO:2.
9. The purified polypeptide of Claim 8 having isoleucine at amino acid residue 121.
10. An antibody specific for the polypeptide of Claim 8.
11. A method for producing MMLR-CCR polypeptide having the amino acid sequence as depicted in SEQ ID NO:2, said method comprising the steps of:
20 a) culturing the host cell of Claim 6 under conditions suitable for the expression of said polypeptide; and
b) recovering said polypeptide from the host cell culture.
12. A method of screening a plurality of compounds for specific binding affinity with the polypeptide of Claim 8 or a portion thereof comprising the steps of:
25 a) providing a plurality of compounds;
b) combining the polypeptide of Claim 8 with each of a plurality of compounds for a time sufficient to allow binding under suitable conditions; and
c) detecting binding of said polypeptide of Claim 8 to each of the plurality of
compounds, thereby identifying the compounds which specifically bind said polypeptide of
30 Claim 7.
13. A diagnostic composition for the identification of MMLR-CCR polypeptide sequences comprising the antibody of Claim 10.
14. A method for inhibiting the expression of MMLR-CCR in a cell comprising

administering an effective amount of the antisense molecule of Claim 4 to said cell.

15. The method of Claim 14 where said cell is in vivo.
16. A purified polynucleotide comprising a nucleic acid sequence encoding the polypeptide
- 5 having the sequence as depicted in SEQ ID NO:4.
17. The polynucleotide of Claim 16 wherein the polynucleotide sequence comprises SEQ ID NO:2.
18. An antisense molecule comprising the complement of the polynucleotide of Claim 16 or a portion thereof.
- 10 19. An expression vector comprising the polynucleotide of Claim 16.
20. A host cell transformed with the expression vector of Claim 19.
21. A diagnostic composition for the detection of mphg-ccr polynucleotide sequences comprising the polynucleotide of Claim 16, or a fragment thereof.
22. A purified polypeptide comprising the amino acid sequence as depicted in SEQ ID NO:4.
- 15 23. An antibody specific for the polypeptide of Claim 22.
24. A method for producing MPH-G-CCR polypeptide having the amino acid sequence as depicted in SEQ ID NO:4, said method comprising the steps of:
 - a) culturing the host cell of Claim 20 under conditions suitable for the expression of said polypeptide; and
 - 20 b) providing a plurality of compounds;
 - b) combining the polypeptide of Claim 21 with each of a plurality of compounds for a time sufficient to allow binding under suitable conditions; and
 - c) detecting binding of said polypeptide of Claim 21 to each of the plurality of compounds, thereby identifying the compounds which specifically bind said polypeptide of
 - 25 Claim 21.
26. A diagnostic composition for the identification of MPH-G-CCR polypeptide sequences comprising the antibody of Claim 23.
27. A method for inhibiting the expression of MPH-G-CCR in a cell comprising administering an effective amount of the antisense molecule of Claim 18 to said cell.
- 30 28. The method of Claim 27 where said cell is in vivo.

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5' ACA AGA TGG ATT ATC AAG TGT CAA GTC CAA TCT ATC ACA TCA ATT ATT ATA TAT
 9 18 27 36 45 54
 M T S I I I Y
 CGG AGC CCT GCC AAA AAT ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC CTG CCT
 63 72 81 90 99 108
 R S P A K K I N V K Q I A A R L L P
 117 126 135 144 153 162
 CCG CTC TAC TCA CTG GTT TTC ATC TTT GGT TTT GTG GGC AAC ATG CTG GTC ATC
 171 180 189 198 207 216
 P L Y S L V F I F G F V G N M L V I
 CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG ACT GAC ATC TAC CTG CTC
 225 234 243 252 261 270
 L I L I N C K R L K S M T D I Y L L
 AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT CTT ACT GTC CCC TTC TGG GCT CAC
 279 288 297 306 315 324
 N L A I S D L F F L T V P F W A H
 TAT GCT GCC GCC CAG TGG GAC TTT GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG
 333 342 351 360 369 378
 Y A A A Q W D F G N T M C Q L L T G
 CTC TAT TTT ATA GGC TTC TTC TCT GGA ATC TTC ATC ATC CTC CTG ACA ATC
 387 396 405 414 423 432
 L Y F I G F F S G I F I I L L T I
 GAT AGG TAC CTG GCT GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG AGC GTC
 D R Y L A V V H A V F A L K A R T V

FIGURE 1A

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441 ACC TTT GGG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT 486
 T F G V V T S V I T W V V A F A S 540
 495 CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC ACC TGC
 L P G I I F T R S Q K E G L H Y T C 594
 549 AGC TCT CAT TTT CAT ACA TTA AAG ATA GTC ATC TTG GGG CTG GTC CTG CCG CTG
 S S H F H T L K I V I L G L V L P L 648
 603 CTT GTC ATG GTC ATC TGC TAC TCG GGA ATC CTA AAA ACT CTG CTT CGG TGT CGA
 L V M V I C Y S G I L K T L L R C R 702
 657 AAT GAG AAG AAG AGG CAC AGG GCT GTG AGG CTT ATC TTC ACC ATC ATG ATT GTT
 N E K K R H R A V R L I F T I M I V 756
 711 TAT TTT CTC TTC TGG GCT CCC TAC AAC ATT GTC CTT CTC CTG AAC ACC TTC CAG
 Y F L F W A P Y N I V L L L N T F Q 810
 765 GAA TTC TTT GGC CTG AAT AAT TGC AGT AGC TCT AAC AGG TTG GAC CAA GCT ATG
 E F F G L N N C S S N R L D Q A M 864
 819 CAG GTG ACA GAG ACT CTT GGG ATG ACG CAC TGC TGC ATC AAC CCC ATC ATC TAT
 Q V T E T L G M T H C C I N P I I Y 855

FIGURE 1B

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873 882 891 900 909 918
 GCC TTT GTC GGG GAG AAG TTC AGA AAC TAC CTC TTA GTC TTC CAA AAG CAC
 A F V G E K F R N Y L V F Q K H
 927 936 945 954 963 972
 ATT GCC AAA CGC TTC TCC AAA TGC TGT TCT ATT TTC CAG CAA GAG GCT CCC GAG
 I A K R F C K C C S I F Q Q E A P E
 981 990 999 1008 1017 1026
 CGA GCA AGC TCA GTT TAC ACC CGA TCC ACT GGG GAG CAG GAA ATA TCT GTG GGC
 R A S S V Y T R S T G E Q E I S V G
 1035 1044 1053 1062 1071 1080
 TTG TGA CAC GGA CTC AAG TGG GCT GGT GAC CCA GTC AGA GTT GTG CAC ATG GCT
 L
 1089 1098 1107 1116 1125 1134
 TAG TTT TCA TAC ACA GCC TGG GCT GGG GGT GGG GTG GGA GAG TCT TTT TTA AAA
 1143 1152 1161 1170 1179 1188
 GGA AGT TAC TGT TAT AGA GGG TCT AAG ATT CAT CCA TTT ATT TGG CAT CTG TTT
 1197 1206 1215 1224 1233 1242
 AAA GTA GAT TAG ATC TTT TAA GCC CAT CAA TTA TAG AAA GCC AAA TCA AAA TAT
 1251 1260 1269 1278 1287 1296
 GTT GAT GAA AAA TAG CAA CCT TTT TAT CTC CCC TTC ACA TGC ATC AAG TTA TTG
 1305 1314 1323 1332 1341 1350
 ACA AAC TCT CCC TTC ACT CCG AAA GTT CCT TAT GTA TAT TTA AAA GAA AGC CTC
 1359 1368 1377 1386 1395 1404
 AGA GAA TTG CTG ATT CTT GAG TTT AGT GAT CTG AAC AGA AAT ACC AAA ATT ATT

FIGURE 1C

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1413	1422	1431	1440	1449	1458
TCA GAA ATG TAC AAC TTT TTA CCF AGT ACA AGG CAA CAT ATA GGT TGT AAA TGT					
1467	1476	1485	1494	1503	1512
GTT TAA AAC AGG TCT TTG TCT TGC TAT GGG GAG AAA AGA CAT GAA TAT GAT TAG					
1521	1530	1539	1548		
TAA AGA AAC GAC ACT TTT CAT GTG TGA AAA AAA AAA AAA AAA A 3'					

FIGURE 1D

[illegible]

FIGURE 2A

201	FHT	IMRN	IUGLVLP	LL	IMVICYSGILK	TLLRCRNEKKRRH	MPiR.g472558	240
173	FHT	LKIV	ILGLVLP	LL	VMVICYSGILK	TLLRCRNEKKRRH	478861	

241	AVR	V	I	F	T	I	M	I	V	Y	F	L	F	W	T	P	Y	N	I	V	I	L	L	N	T	F	Q	E	F	F	G	L	S	N	C	E	S	T	MPiR.g472558	280
213	AVR	L	I	F	T	I	M	I	V	Y	F	L	F	W	A	P	Y	N	I	V	I	L	L	N	T	F	Q	E	F	F	G	L	N	N	C	S	S	478861		

281	S	Q	L	D	Q	A	T	Q	V	T	E	T	L	G	M	T	H	C	C	I	N	P	I	I	Y	A	F	V	G	E	K	F	R	R	Y	L	S	V	F	F	MPiR.g472558	320
253	N	R	L	D	Q	A	M	Q	V	T	E	T	L	G	M	T	H	C	C	I	N	P	I	I	Y	A	F	V	G	E	K	F	R	N	Y	L	L	V	F	F	478861	

321	R	K	H	I	T	K	R	F	C	K	Q	C	P	V	F	Y	R	B	T	V	D	G	V	T	S	T	N	T	P	S	T	G	E	Q	E	V	S	A	G	L	MPiR.g472558	360
293	Q	K	H	I	A	K	R	F	C	K	C	C	S	I	F	Q	Q	E	A	P	E	R	A	S	S	V	Y	T	R	S	T	G	E	Q	E	I	S	V	G	L	478861	

FIGURE 2B

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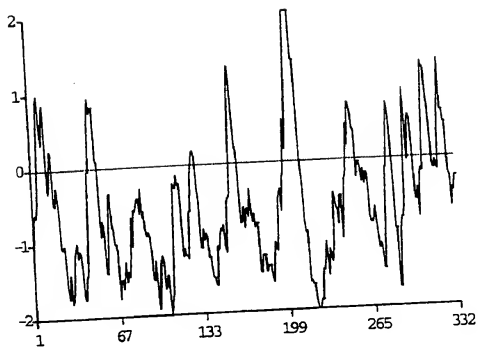


FIGURE 3

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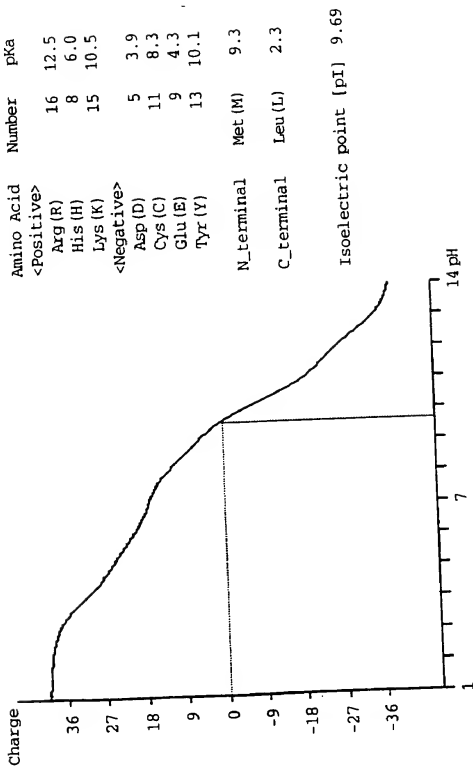
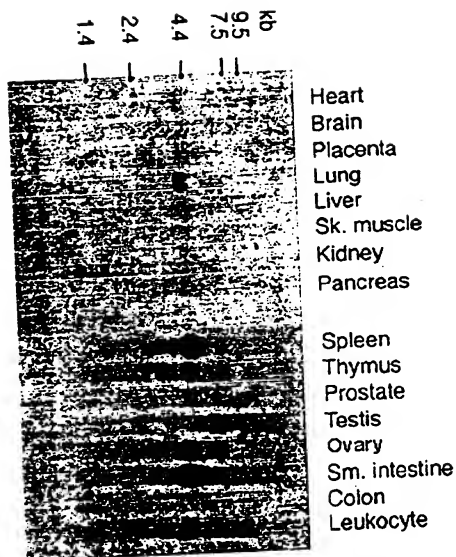


FIGURE 4

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**FIGURE 5**

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180 189 198 207 216
 ATG GCC AAT TAC ACG CTG GCA CCA GAG GAT GAA TAT GAT
 Met Ala Asn Tyr Thr Leu Ala Pro Glu Asp Glu Tyr Asp
 234 243
 225 234 243
 GTC CTC ATA GAA GGT GAA CTG GAG AGC GAT GAG GCA CAA TGT GAC AAG TAT
 Val Leu Ile Glu Gly Glu Leu Ser Asp Glu Ala Glu Gln Cys Asp Lys Tyr
 279 288 297 306 315 324
 GAC GCC CAG GCA CTC TCA GCC CAG CTG CTG CCA TCA CTC TGC TCT GCT GTG TTT
 Asp Ala Gln Ala Leu Ser Ala Gln Leu Val Pro Ser Leu Cys Ser Ala Val Phe
 333 342 351 360 369 378
 GTG ATC GGT GTC CTG GAC AAT CTC CTG GTT GTG CTT ATC CTG GTA AAA TAT AAA
 Val Ile Gly Val Leu Asp Asn Leu Leu Val Val Leu Ile Leu Val Lys Tyr Lys
 387 396 405 414 423 432
 GGA CTC AAA CGC GTG GAA AAT ATC TAT CTT CTA AAC TTG GCA GTT TCT AAC TTG
 Gly Leu Lys Arg Val Glu Asn Ile Tyr Leu Leu Asn Leu Ala Val Ser Asn Leu
 441 450 459 468 477 486
 TGT TTC TTG CTT ACC CTG CCC TTC TGG GCT CAT GCT GGC GAT CCC ATG TGT
 Cys Phe Leu Leu Thr Leu Pro Phe Trp Ala His Ala Gly Gly Asp Pro Met Cys
 495 504 513 522 531 540
 AAA ATT CTC ATT GGA CTG TAC TTS CTG GGC CTG TAC AGT GAG ACA YTT TTC AAT
 Lys Ile Leu Ile Gly Leu Tyr Phe Leu Gly Leu Tyr Ser Glu Thr Xxx Phe Asn
 549 558 567 576 585 594
 TGC CTT CTG ACT GTG CAA AGG TAC CTA GTG TTT TTG CAC AAG GGC AAC TTT TTC
 Cys Leu Leu Thr Val Gln Arg Tyr Leu Val Phe Leu His Lys Gly Asn Phe Phe

FIGURE 6A

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603 TCA GCC AGG AGG AGG GTG 612 621 630 639 648
 Ser Ala Arg Arg Arg Val Pro Cys Gly Ile Thr Ser Val Leu Ala Trp Val
 657 ACA GCC ATT CTG GCC ACT TTG CCT GAA TAC GTG GTT TAT AAA CCT CAG ATG GAA
 Thr Ala Ile Leu Ala Thr Leu Pro Glu Tyr Val Val Tyr Lys Pro Gln Met Glu
 711 720 729 738 747 756
 GAC CAG AAA TAC AAG TGT GCA TTT AGC AGA ACT CCC TTC CTG CCA GCT GAT GAG
 Asp Gln Lys Tyr Lys Cys Ala Phe Ser Arg Thr Pro Phe Leu Pro Ala Asp Glu
 765 774 783 801 810
 ACA TTC TGG AAG CAT TTT CTG ACT TTA AAA ATG AAC ATT TCG GTT CTT GTC CTC
 Thr Phe Trp Lys His Phe Leu Thr Leu Lys Met Asn Ile Ser Val Leu Val Leu
 819 828 837 855 864
 CCC CTA TTT ATT TTT ACA TTT CTC TAT GTG CAA ATG AGA AAA ACA CTA AGG TTC
 Pro Leu Phe Ile Phe Thr Phe Leu Tyr Val Gln Met Arg Lys Thr Leu Arg Phe
 873 882 891 900 909 918
 AGG GAG CAG AGG TAT AGC CTT TTC AAG CTT GTT TTT GCC ATA ATG GTA GTC TTC
 Arg Glu Gln Arg Tyr Ser Leu Phe Lys Leu Val Phe Ala Ile Met Val Val Phe
 927 936 945 954 963 972
 CTT CTG ATG TGG GCG CCC TAC AAT ATT GCA TTT TTC CTG TCC ACT TTC AAA GAA
 Leu Leu Met Trp Ala Pro Tyr Asn Ile Ala Phe Phe Leu Ser Thr Phe Lys Glu
 981 990 999 1008 1017 1026
 CAC TTC TCC CTG AGT GAC TGC AAG AGC AGC TAC AAT CTG GAC AAA AGT GTT CAC
 His Phe Ser Ser Leu Ser Asp Cys Lys Ser Tyr Asn Leu Asp Lys Ser Val His

FIGURE 6B

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1035	1044	1053	1062	1071	1080
ATC ACT AAA	CTC ATC GCC ACC	ACC CAC	TGC ATC	RAC CCT	CTC CTG TAT GCG
Ile Thr Lys	Leu Ile Ala Thr	His Cys	Ile Asn	Pro Leu	Leu Tyr Ala
1089	1098	1107	1116	1125	1134
TTT CTT GAT	GCG ACA TTT	AGC AAA	TAC CTC	TGC TGT	TTC CAT CTG CGT AGT
Phe Leu Asp	Gly Thr Phe	Ser Lys	Tyr Leu	Cys Arg	Cys Phe His Leu Arg Ser
1143	1152	1161	1170	1179	1188
AAC ACC CCA	CTT CAA CCC	AGG GGG	CAG TCT	GCA CAA	GGC ACA TCG AGG GAA GAA
Asn Thr Pro	Leu Gln Pro	Arg Gly	Gln Ser	Ala Gln	Gly Thr Ser Arg Glu Glu
1197	1206				
CCT GAC	CAT TCC	ACC GAA	GTG TAA	3'	
Pro Asp	His Ser	Thr Glu	Val *		

FIGURE 6C

FIGURE 7A

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191	T	V	S	W	R	H	F	H	T	L	R	M	T	I	F	C	L	V	L	P	L	V	M	A	I	C	V	T	G	I	I	K	T	L	-	L	R	C	CCR3.g881570		
193	E	T	F	-	W	K	H	F	L	T	L	K	M	N	I	S	V	L	V	L	P	L	F	I	F	T	F	L	V	Q	M	R	K	T	L	R	F	B	-	442279	
231	P	S	K	K	K	Y	K	A	I	R	L	I	F	V	I	M	A	V	F	F	I	F	W	T	P	Y	N	V	A	I	L	L	S	Y	Q	S	I	L	F	CCR3.g881570	
231	-	-	E	Q	R	Y	S	L	F	K	L	V	F	A	I	M	V	V	F	L	L	M	A	P	Y	N	I	A	F	F	L	S	T	F	K	E	H	F	S	442279	
270	G	N	D	C	E	R	S	K	H	L	D	L	V	M	L	V	T	E	V	I	A	Y	S	H	C	C	M	N	P	V	I	Y	A	F	V	G	E	R	F	CCR3.g881570	
269	L	S	D	C	K	S	Y	N	L	D	K	S	V	H	I	T	K	L	I	A	T	T	H	C	C	I	N	P	L	L	Y	A	F	L	D	G	T	F	S	442279	
310	K	Y	L	R	H	F	F	H	R	H	L	M	H	L	G	R	Y	I	F	F	L	P	S	E	K	L	E	R	T	S	S	V	S	P	S	I	T	A	E	P	CCR3.g881570
309	K	Y	I	C	R	C	F	H	-	-	-	-	-	L	R	S	N	T	P	L	Q	P	R	Q	-	-	-	S	A	Q	G	T	S	R	E	E	P	442279			

FIGURE 7B

CCR3.g881570
442279

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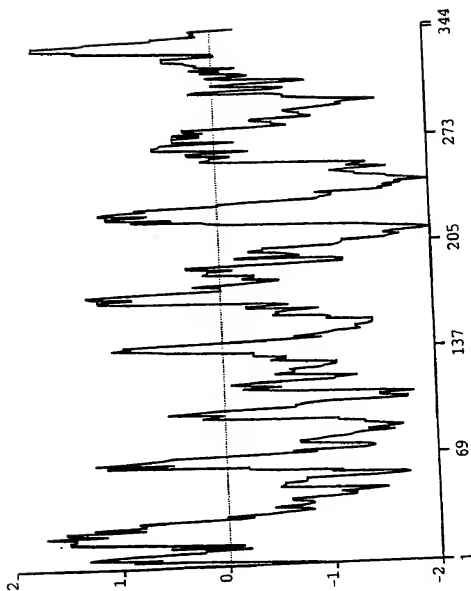


FIGURE 8

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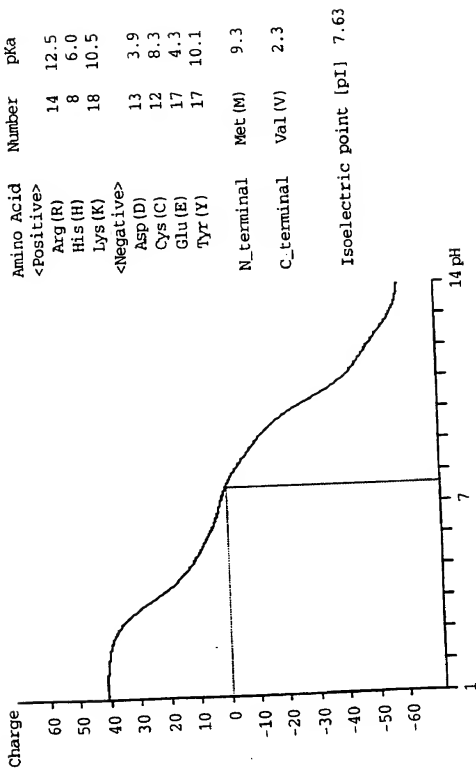


FIGURE 9